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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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## - nucleic search, isting account police police models OM protein

April 6, 2006, 09:51:12; Search time 6373 Seconds (without alignments) 3380.459 Million cell updates/sec US-10-780-703-2 2034 Title: Perfect score: Run on:

1 MAIVSSTTSIIPMSNQVNNN.........MWNPIVPDGNRDHYTNIPFK 379 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Sequence:

5883141 segs, 28421725653 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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GenEmbl: \* Database :

gb ba: gb\_ro:\*
gb\_sts:
gb\_sy:\*
gb\_un:\*
gb\_vi:\*
gb\_htg: 90

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	G	BT000874 Arabidops	AC005312 Arabidops	AF360308 Arabidops	
ID		100.0 1171 15 BT000874	AC005312	AF360308	
DB		72	15	15	
Query Match Length DB	, ;	1171	74903	1062	
Query		100.0	85.3	77.4	
Score		2034	1735	1574	
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4	815.5		-		AK102902	2 Oryza
D.	796.5		16	15	AK072275	75 Oryza
i Qu	796.5		- 0	s i	AK071052	52 Oryza
- 0	789.5				AK068393	
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٠.	769 5			4	A4654030 2007649	Avestus Sequence
11	769.5			. 4	AP007409	1 Totus
12	759		1250	9	AX654570	Sequenc
13	688.5			9		Sequence
14	672.5			.12	اں ا	
15	672.5			15	38	387
1 T	672.5			ל ה	AP003346 AB003431	APOUSS46 Oryza sat
1	655.5		110000	15	AP008211 203	tion (2
c 19	655.5	32		15	١.	AC137623 Oryza Bat
20	611			15	AP008214_007	Continuation (8 of
21	611		18	15	AP005657	AP005657 Oryza sat
22	5250				AK107090	AKI07090 Oryza sat
24	544.5			9	AX654270	oryza sa leguence
25	536			9	AX653803	AX653803 Sequence
. 56	517.5				AX652795	AX652795 Sequence
27	517			in a	AY573802	AY573802 Lycopersi
200	516			n u	DQ028772	DQ028//2 GIYCine m
3.0	514			n	AF301804 AX651430	
3.5	514			'n	D0028774	DO028774 Glycine m
32	512			ın	AF011555	
33	512				AJ704829	AJ704829 Prunus pe
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37	508.5			S LO	BT008346	Arabidop
38	508.5	•		9	CS137954	S.
39	508.5			12	AK117878	- 1
40	508		68	9	CS137686	9
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4 4	200		- ۱	1 5	AF083738	33738
45	508	25.0	123	15	7.7	72 Arabidop
					ALIGNMENTS	
RESULT 1 BT000874						
LOCUS		BT000874 Arabidopsi	is thaliana	ana	71 bp mRNA C104984 putative	linear · PLN 16-OCT-2002 NAM (no apical
0.000		meristem)	protein	A.	(At2g02450) mRNA, complete	cds.
VERSION			GI:24030185	0301	85	
SOTTECE	7 L L	Arabidoneie	e thaliana	מ	(thale cress)	
ORGANISM		Arabidopsis	s thaliana	ana	)	
		karyota	. Viridiplantae;	plan	tae; Streptophyta; Embry	ophyta; Tracheophyta;
	Sp	ermatop	yta; Mag	gnol	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons	core eudicotyledons;
	Ñ	sids; en	rosids	II;	Brassicales; Brassicacea	<ul><li>a) Arabidopsis.</li></ul>

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases 1 to 171)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M.,
Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,
Ecker, J.R., and Theologis, A. Unpublished
Z. (Dases 1 to 1171)
Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M.,
Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
Ecker,J.R. and Theologis,A. TITLE JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS

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AC005312
Arabidopsis thaliana chromosome 2 clone T16F16 map CIC11A04, complete sequence.
AC005312, GI:20197334
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases I to 74903)
Rounsley, S.D., Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Mason, T.M.,
Shen, M., Ronning, C.M., Fraser, C.M., Somerville, C.R., and Venter, J.C.
Unpublished
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Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpAsnProlleValProAspGlyAsnArgAspHisTyrThrAsnIleProPheLys 379
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                                                  141 IleargSerGluThrSerArgProlleGlyLeuLysLysThrLeuValPheTyrSerGly
                                                                       LysAlaProLysGlyThrArgThrSerTrpIleMetAsnGluTyrArgLeuProHisHis
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AC005312
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                     /product = putative NAM (no apical meristem) protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVTIALANQNIYRPMPYDTSNNTLIVSTRNHQDDDETAIVDDLQRLVNYQISDGATTL
     Direct Submission
Submitted (16-OCT-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
Annotation based on January 2002 version of the Arabidopsis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLy8Gly1leGluAspAsnAspHisArgGlyGlyGlnGluSerHisValGlnAsnGlu 40
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379
0
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                       organism="Arabidopsis thaliana"
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COMMENT

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//mnc=18.7002080. .17046)
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paeggglldcdbivlsvididyaywkcgliiqgidirptksp"
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gomplement (join(16098. .16334,16849. .17046))
complement (join(16098. .16334,16849. .17046))
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db_xref="GI:3894160"
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                                                                                                                                                                                                                                                           protein"
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/rpc_family="AT_rich"
complement(17280...17307)
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complement (17834. 17896)
/rpt family-"AT rich"
complement (18077. 18151)
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                                                 complement (10262. .11417)
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                           'pseudo
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THOFFGGI PRELANSFELLNLLNRRNBELSGRLMCTPANIALANSLDLCTFYRFNGRELPB
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TTLVLTLNFHGEALPDDSSLHPEKLKVLVVANCRLTGSMPRWLSSSNELQLLDLSWNR
TTLATAFTREUTSRNSFYRSTGSIPKSFTNTESLTSRXISVNESSPEPFRK
RNEGARALQYNQIFGFPFI ELGHNNLSGPTBEFKNLKLELTFFRISVISVNERSEPPFRK
RNEGARALQYNQIFGFPFI ELGHNNLSGSTFREFKSVATVNLSGVIPSGGFGFFPSS
LSGMTSLEALDLSNNRFKSSIPVSLQQLSFLSKFSVATVNLSGVIPSGGGFGFFPSS
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VYFESGNADSRSATSHYSGISEEEEEVEGERERGMNVVGPKERVDGWSEVELGKFYIN
NGGCGDDGSDEIEISIMETQNGNWKSGLIIQGIEIRPERSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRVHRFCVIVIFLTELLCFPYSSESQTTSRCHPHDLEALRDFIA
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GSLPSHICHNGTQIPTAVWLANYRFAGNFISGFGKCVLLBHLCLGMNDLTGNIPEDLFH
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GCGGFGMVYKATLPDGKKVAIKKLSGDCGQIEREFEAEVETLSRAQHPNLVLLRGFCF
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SHTSPRDACVVASVSKSVKSAAQSDLVWEMFLPSEYSSLVLQSANHLSKKE1FLSLAD
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/gene="At2g02240"
/note="synonym: T16F16.3; pseudogene, phloem-specific
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6867. .>7202))
3 (bases 1 to 74903)
Town.C.D. and Kanl,S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9
Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598458.
Location/Qualifiers
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6867. .7202))
/gene="At2g02230"
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/protein_id="AAC78507.3"
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complement(<1. .>2731)
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complement(35047.3524)
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complement(4101. .4133)
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complement(6000. 720
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                                                                                                                                                                    -- AlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyr
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GCYDYAQLVLEMIDPDKIYFCRRESPESELIKLRSFVHQFLKECNEMFSLIVVTIK
GCYDYAQLVLEMIDPDKIYFCRRESPESELIKLRSFVHQFLKECNEMFSLIVVTDKSSVWPH
DLUSVUVRPLLKEISLRKKRKADGVV"
COMPLEMENT (218 SIRWKRKADGVV"
/gene="at2g02300"
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FIVDNYQGRSFDYLYTGIQMSNEALGFTKRLISQTSWLEDKKLHLVLDLDHTLVHTIK
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                                                                                                 note="synonym: T16F16.8; predicted by genscan and
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'protein id="AAC78513.1"
'db_xref="GI:3894163"
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complement(join(<22168. .22558,22680.
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product="hypotein"
'protein_id="AAC78512.1"
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The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satch,K., Nagata,T., Kawagashira,N., Doi,K., Kikuchi,S., Satch,K., Onda,E., Yahagi,W., Yamada,H., Hutta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Li,C., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Li,C., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Li,C., International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Kurosaki,T., Kodama,T., Maeuda,H., Kobayashi,M., Xie,O., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kawai,J., Carninci,P., Adachi,J., Alazawa,K., RikER:, Kagawa,I., Konda,M., Matsubara,K., RikER:, Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino, mapping, and annotation of over 28,000 cDNA clones from
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                                                                                                                                                                                                                                                      AK102902 1631 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone:J033113D13, full
insert sequence.
AK102902
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                                                                                                                                                                                                                                                                                                                                                            FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
  723 TCAGATGGAGCGACACGCTAATGCCTCAAACTCAAGCGGCGTTAGCTATGAACATGATT
                                                                  783 CCTGCAGGAACGATTCCAAACAATGCTTTGTGGGATATGTGGAATCCAATAGTACCAGAT
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Oryza sativa (japonica cultivar-group) cDNA clone:J023012F04, full
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                                                  uThrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLysArgProGlyVa
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                     URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIASA Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Ishikawa,M., Yazadahira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M.
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033113D13"
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Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J. Ishikaw, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fulimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawanata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayateu, N., Imocani, K., Ishii, Y., Icho, M., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, J., Yoshino, M. and Hayashizaki, Y., Solino, M. and Hayashizaki, Y., Solino, M. and Hayashizaki, Y., Solino, M., Shiraki, T., Solino, A., Ishi, M., Shiraki, T., Solino, A., Ishi, Sato, R., Salio, 
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NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Obheda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.
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Rudama,T., Kurosaki,T., Kusumana,M., Kobayashi,M.,
Rodama,T., Kurosaki,T., Kusumagi,T., Lu,M., Masuda,H., Mura,J.,
Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Matsubara,K. and Murakami,K., Ye,O., Yokomizo,S.,
Yoshimura,A., Matsubara,R. and Murakami,K.,
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Haraak,A., Hashizune,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Iltoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
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Kishikawa-Hirozane, T., Kojina, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Momura, K., Numasaki, R., Ohno, M., Osato, N.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazune, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
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Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
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                                                                      (japonica cultivar-group)"
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/organism="Oryza sativa (j
/nol_type="nRNN"
/cultivar="NIpponbare"
/db xref="taxon:39947"
/clone="J023012F04"
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Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohned,E., Ohno,M., Ohtsuki,K., Nomura,K., Sato,N., Ota,Y., Otomo,Y., Ryul, Sattoh,H., Sakai,C., Sakai,K., Shinagawa,A., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shizuki,K., Suzuki,Y., Tagami,M., Tagami,Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tamunoda,Y., Ueda,M., Waki,K., Xie,Q., Yanaqai,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and	Yoshimura, A.  TITLE Direct Submission JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007, This Clone is one of the 28K full-length CDNA Clones from Japonica		Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Mura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Teunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiracka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kanai,Y., Kolima,Y., Konno,H., Kowai,J., Koliha,Y., Kurihara,M., Kulihara,M., Nishi,K., Nomura,K., Numasaski,R., Ohno,M., Osato,N.,	Otal'r, Saltoh.H., Sakal,C., Sakal,R., Sakacume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Sho,H., Sagabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomatu,A., Toya,T., Waki,K., Taskatu-Akahira,A., Tanaka,T., Tomatu,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.  Location/Qualifiers    Lagai   Lagai   Corganism="Oryza sativa (japonica cultivar-group)"   mol type="mRNA"   /mol type="mRNA"	Alignment Scores: Pred. No.: Pred. No.: Pred. No.: Pred. No.: Score: Score: Parcent Similarity: 55.9\$ Matches: Percent Similarity: 44.6\$ Mismatches: 101 Best Local Similarity: 15. Matches: 177 Conservative: 45 Mismatches: 101 Best Local Similarity: 15. Mismatches: 101 Best Local Similarity: 15. Mismatches: 16  Mismatches: 177  Gaps: 16  Mismatches: 16  Mismatches: 16  Mismatches: 177  Mismatches: 16  Mismatches: 16  Mismatches: 177  Gaps: 16  Mismatches: 16  Mismatches: 177  Mismatches: 16  Mismatches: 177  Mismatches: 16  Mismatches: 16  Mismatches: 177  Mismatches: 16  Mismatches: 177  Mismatches: 174  Mismatches: 177  Mismat
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ò	GluThrSerArgProIleGlyLeuLySLysThrLeuValPheTyrSerGlyLysAlaPro
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	164 LysGlyThrArgThrSerTrpIleMetAsnGluTyrArgLeuProHisHisGluThrGlu 183
qa	724 AAGGGGTTCGCAGCAGCTGGATCATGAACGAGTATCGTCCCTCATGGCGACGCTGAC 783
č	184 LysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLysArgProGlyValGluAsp 203
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qq	901 GGCAAGAAGCACGCCGCCGAACCGGACGTCATCGACGGCGGCGGCGGCGCCCCCCCC
	230 GlnGlnGln 236
qq	961 CTCGCCCCGATGTTCGACGGCGGCGGCGGCGCCCACCATCCGCCCTCATGGGAAAG 1020
	237SerSerAsnHisSerAspAsnAsnAsnAsnAsnAsnAsnAsnIle 251
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Db 1	1081 TCGGCGGCGGCGCGCTGCATCCTCCGGCGCCGGCGATGTTCCGGTCGACGGCGTCGGTG 1140
à	252AsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAsp 264
Db 1	1141 GCCTCGCTGAGCTCCACCACCACGAGGAGGAGGACGACGCACGTCGCTCTTCCACCTCAAG 1200
&	265GlySerThrThrThrThrThrAsnSerAsnSerAspValThrIleAlaLeuAla 283
. do	1201 GCCGGCGCGACGACGACGACGACGACGACGACGACGACGA
λ̈́o	284 AsnGlnAsnIleTyrArgProMetProTyrAspThrSerAsnAsn 298
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Š	299 ThrLeulleValSerThrArgAsnHisGlnAspAspAspGluThrAlalleValAspAsp 318
Db 1	1297 TCAGCAATGGCG
ò	319 LeuGlnArgLeuVal328
Db 1	1327 CTGAGTAGGGCGATTGGATCTTACAGCAACATCCACCATCAACCTACAACT 1386
Š	329 AspGlyAlaThrThrLeuMetProGlnThrGlnAlaAlaLeuAlaMetAsnMetIlePro 348
Db 1	1387 CATCAATCAACTGCTTTGCCGCCATCGCAACAAGCCCTCTTCTTCCA 1434
È	349 AlaGlyThrIleProAsnAsnAlaLeuTrpAspMetTrpAsnProIleVal 365
Dp 1	1435 TTCGCTAGCATGGAGAAGATTGGGATTGGAACCCTCTCTA 1476

The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugamo, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Iida, Y., Sugamo, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Yoshimura, A., Miura, J., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidune, W., Hayatsu, M., Imotami, K., Ishii, Y., Itch, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Saski, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshimo, and Hayashizaki, Y.
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Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and

Voshimura, A. rice.
URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Saroh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Pujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., AK068393 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J013151L09, full Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica AKO68393.1 GI:32978411

PLJ CDNA, CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Enrhartoideae, Oryzeae, Oryza. Direct Submission insert sequence foshimura, A. RESULT 7 AK068393 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM PUBMED REFERENCE AUTHORS TITLE JOURNAL ACCESSION AUTHORS JOURNAL REFERENCE TITLE COMMENT

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Hordeum vulgare subsp. vulgare NAC transcription factor mRNA, AY672069
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Hordeum vulgare subsp. vulgare
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Hordeum.
1. (bases 1 to 1406)
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Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
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Yoshimura,A., Matsubara,K. and Murakami,M. Xie,Q., Yokomizo,S.,
and Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
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Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitch,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
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Yasunishi,A. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLysGluTrpTyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArgPro 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 GACAAGAGTGGTTCTTCTATGTGCCAAGGGACGCAAGTACCGAAACGGCGATCGGCCC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAlaAspArgMetIleArgSer 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluThrSerArgProIleGlyLeuLysLysThrLeuValPheTyrSerGlyLysAlaPro 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 AACCGAGTGACGCCATCGGGGTACTGGAAGGCCACAGGGGCGGATAGGATGGTGAAGGTG 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 GACGGGCAGGCGCACGACGATGGTGATGCCGGGGTTCCGGTTCCACCCGACGGAGGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2424
175
46
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101
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1002 GGCGACCATCCCGATCGACGAGTGAGTCGGGCGATTGGGTCCTACAGTCAAGCTTCAAA 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                           -----GCGCACACGACCCA 773
                                                                                                                                                                                                                                                                                                                                                                     560 AGCACACCGGACGICAGCGGIGGCAACTCACCGCCAGCAGCCGCCAGTGTTTGTCGAAGG
                                                                                                                                             250 nileAsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAspGlySerThrThrTh
                                                                                                                                                                                                                                                                    oMetProTyrAspThrSerAsnAsnThrLeuIleValSerThrArgAsnHisGlnAspAs
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                                                233 -----HisHisSerSerSerAsnHisSerAspAsnAsnLeuAsnAsnAsnAs
                                                                                                                                                                                                                                           270 rThrThrAsnSerAsnSerAspValThrIleAlaLeuAlaAsnGlnAsnIleTyrArgPr
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185
47
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81
                                                                           720 CGCCGGTCACCACTCATCATCTGCTCTCAAGGCGTACAAC----
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Matches:
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Mismatches:
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Sequence 3920 from Patent W003000898.
AX654050 GI:29156864
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Pred. No.:
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AUTHORS
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JOURNAL
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AX654050
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TIPIDELSRAIGSYSQASNPNQPTAPMQGPLLNFPSLEKIWDWNPLLESPKVCTSFK"
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181
54
82
93
                                                                         /note="HSINAC; HvSPY-interacting NAC"
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Matches:
Conservative:
Mismatches:
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Gaps:
                              db_xref="taxon:112509"
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FEATURES *	70428 70527: gap of unknown length 70528 80577: contig of 10050 bp in length. Location/Oullifiers	qq	35989 ITCAITTICCACGCCGCCTCCTCTTCTCCCTTTTTTCTGCCAICTATCTCCCTTCAA 36048
sonrce		ò	97
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gap	2102220] /estimated length-unknown	ځ	98AlaMetAlaAlaIleGlvGlvLvsGl 106
gap	3131. 3230 Jastinated Jenethambrown	;	
gap	43374436	3 ,	
gap	/estimated_length=unknown 6410, .6509	ò ·	uTrpiyrPheiyrva.lrroargasparguyeiyrargashu1yAspargkroashargva 126
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dap	/estimated_length=unknown 1136711466	ò	126 1ThrThrSerGlyTyrTrpLySAlaThrGlyAlaAspArgMetIleArgSerGluThrSe 146
a de	/estimated.length=unknown 1448414583	q	
և ն 1 ն	/estimated length-unknown	ò	146 rArgProlleGlyLeuLysLysThrLeuValPheTyrSerGlyLysAlaProLysGlyTh 166
gap	1835118560 /estimated_length=unknown	qa	36409 CAGGICAATTGGGCTGAAGAAAACCCTAGTTTTCTATTCTGGGAAAGCTCCCAAAGGCAT 36468
gap	2585325952 /estimated_length=unknown	ò	166 rArgThrSerTrpIleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGl 186
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. <u>.</u>		ф	36529 AAAGGTACCGTACACACACAAATCTACTTACCATGAAGACGTACACTCAGAATCAATT 36588
d d d	/estimated_length=unknown	ò	186 186
ORIGIN		QQ	36589 ATTAAACTCGGAATCTATTTACAGAAGATTTTCCACCAATTCTAAAACTCTAAGAGGATT 36648
Alignment Scores: Pred. No.:	1.33e-48 Length:	ð	186 186
Score: Percent Similarity:	769.50 32.9%	qq	36649 ITAAAAACCTGCAATGTTACACGGGTATTTGATAAAAGCTTTAAAAACCAGTTCTAGTAC 36708
Best Local Simila Query Match:	27.5% Mismatches: 37.8% Indels:	ò	186 186
	14 Gaps:	ą.	36709 ATAGCCTTTTTTGCTCATTCTTCTTCATGAGGTAGCCCAGTCAAAGGTTTAAAATTCA 36768
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	58	Q	36769 ACCCTAGITITAAAGCTATGAICATTAATTCTGTGTCATGTTGGTTTTCCCAGCTCTTTT 36828
35689	ŭ	ò	186 186
59	78	qq	36829 GATAATTCGATCATTAGCAATTGCCATACATAAAATCATCTTAATTTTCTCTCACACAC 36888
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79	AsnValGluLeuileThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuPro 97	q	36889 TTTAAGTAGCAAAATTTAGATCCAAAGCTAGCTATAGCATGCCAAACCAGTAGGTGCGTG 36948
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Oy 97		qq	36949 AAACTCGCAGCCACCATTAAATTTATATTCAAGAGTACTCTTTGCATTTAATAATACT 37008
	ATATATACTATACTATTACACACGCATGTACATACATACA	ò	186 186
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79 VQ	16	ï	

	AUTHORS Sato, Sato, Sato, Sato, Sato, Batcot Submission JOURNAL Submisted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute, JOURNAL Submitted (26-OCT-2004) Shusei Sato, Kazusa DNA Research Institute, Chiba, 292-08194, Japan (B-mail:seato@kazusa.or.jp, URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337), Pax:81-438-52-3935)  * NOTE: This is a 'working draft' sequence. It currently * consists of 24 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence	* as soon as it is available and the accession number will  * be preserved.  * 3414: contig of 3414 bp in length  * 3415	contig of 1773 gap of unknown contig of 2651 gap of unknown contig of 2511 gap of unknown contig of 2365 gap of unknown contig of 1269 gap of unknown contig of 1269 gap of unknown contig of 1368 gap of unknown contig of 1368 gap of unknown contig of 3168 gap of unknown contig of 3168	22863 34190: contid 34191 34290: gap of 34291 34886: contid 34291 38986: contid 43710 43809: gap of 43710 43809: gap of 47836 54444: contid 47936 54444: contid 54445 54444: contid 54545 60454: contid 60555 70888: contid 60555 70888: contid 70889 88088: contid 88089 70988: gap of 60559 70988: gap of 60559 70988: gap of 60550 70988: gap of 60550 70988: gap of 60550 70988: contid 88088: contid 88088: contid 88088: contid 88089 891718: contid 88088: contid
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Db         37069         CTCGAACATATTATGATTACACGCATGAATTGTGAATTCTGACACTCCATGTCTCGTGAC         37128           Qy         186	Oy         193 BARGValTyrLysArgProGlyValGluAspHisProSerValProArgSerLeuSerTh 213           Db         37249 CCGGGTATACAAGAGACTGGAGTAGAAGATCATCCTTCCCTCCTCGTTGTCTCCCAAT 37308           Oy         213 TATGHISHISABNHISABNSETSETTHYSETSERARGLEUALaLeuArgGInGInHi 233           Db         37309 TACCAAGCCATCATCCTCAAGATCATCAAAACCAAGTGAAATAGCTCAGCATCAATA 37368           Qy         233 S	Qy         243 nAsnLeuAsnAsnAsnIleAsnAsnIleAsnAsnIleAsnAsnLeuGluLysEerGluTyrSerGl 263           11	Db 37582 GCCAGCGAGGAGGAGGTTGATGCTCCTGCCGCAGCACTCAATAATCCAAA 37611  Qy 308	Oy 355 nAlaLeuTrpAspMetTrpAsnProllevalProAspGlyAsnArgAspHisTyrThrAs 375

Qy         79 AsnValGluLeuIleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuPro 97           Db         40849 AATGTTGAGCTCATCATTTCCTTGATCTTTATCGCTATGACCCTTGGGAGCTTCCTGGT 40908           Qy         97	Db 40909 ATATATACTATACACACGCATGTACATACATACAAATACAATTATTATT 40968	40969 CADATTIGDAAGCAAGCTICCCTITICTIGAAGCAATTICTIGTAAGAAAATTCATTT	QY 97	Db 41029 TTCATTTTCCACGCCGCCTCCTTTTTTCTCCCATCTATCT	97	41089 TTTTATATTTAACTTTTCTTGATACAACTAGCTAAGGTTTATTTTAATATATAGTTC	97	411	OV ST. ALLOND INCRMINENTS A SIMPLE STATE OF THE SIMPLE STATE OF THE ST		Db 41269 AGCTGAGTTGAATCTATGATGAGGTGCAGCTTTGGCAGCTATTGGTGAGGA 41328	106 ulrpTvrPheTvrValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgVa	41	126	Db 41389 GACTACTTCTGGGTATTGGAAGCAACGGAGCTGACAGGATGATTGGAACTGAAAACTT 41448	Qy 146 rArgProIleGlyLeuLy8LyRThrLeuValPheTyrSerGlyLy8AlaProLysGlyTh 166	Db 41449 CAĞGTCAATTGĞĞCTGAAĞAAAAÇCCTAĞTTTTCTATTCTGĞĞAAAĞCTCCCAAAĞĞCAT 41508	Qy 166 rargThrSerTrplleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGl 186	186	41569 AAAGGTACCGTACACACACAAATCTACTTTACCATGAAGACGTACACTCAGAATCAATT	Oy 186 186	Db 41629 ATTAAACTCGGAATCTATTACAGAAGATTTTCCACCAATTCTAAAACTCTAAGAGGATT 41688	Qy 186 186	Db 41689 TTAAAAACCTGCAATGTTACACGGGTATTTGATAAAAGCTTTAAAAACCAGTTCTAGTAC 41748	Qy 186 186	Db 41749 ATAGCCTTTTTTGCTCATTCTTTCATGAAGCTAGCCCAGTCAAAGGTTTAAAATTCA 41808	Qy 186 186	41809 ACCTAGITTTAAAGCTATGATCATTAATTCTGTGTGTTGGTTTTCCCAGCTCTTT	Db 41869 GATAATTCGATCATTAGCAATTGCCATACATCATAAATCATCTTAATTTCTCTCACACAC 41928
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:::	REPERENCE 1 AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G. TITLE Plant genes involved in defense against pathogens Involved in defense against pathogens Plant genes involved in defense against pathogens Journal Participations AG (CH)  FEATURES Location/Qualifiers  Source / Organism="Oryza sativa" / Ab_xref="taxon:4530" / Ab_	Oy 50 MetValMetProGlyPheArgPheHisProThrcluGluGluLeuIleGluPheTyrLeu 69	Qy         130 GlyTyrTrpLyshlaThrGlyAlaAsphrgMetIleArgSerGluThrSerArgProlle         149           Db         241 GGGTACTGGAAGGCGATAGGATGGTGAAGGTGAGGTGACCGTCCTATC         300           Qy         150 GlyLeuLy8Ly8ThrLeuValPheTyrSerGlyLy8AlaProLy8GlyThrArgThrSer         169           Db         301 GGCTCAAGAAGACGCTCTTCTACGTCGGCAAGGGCGCCAAGGGGCTTCGCAGCAGC         360           Qy         170 TrplleMetAshGluTyrArgLeuProHisHisGluThrGluLy8TyrGlnLy8
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127 ThrThrSerGlyTyrTrDLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSer 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 CGCCCCATCGGCCTCAAGAAGACGCTCGTCTTCTACTCCGGCAAGGCCCCCAAGGGCGTC 468
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Syngenta Participations AG (CH)
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                   GCGAACCGGACGTCATCGACGGCGGGGGGGCGCCCCGCTCGCCCCGATGTTCGAC
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NDLYPGYTLEPPPRFYRFVGFTDLKYBRREYYRPPGEREDKWMEAELGEFFNETSCGDV
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faeggglLDCDE1VLSVIDIDYaYWKCGLIIQGIDIRPTKSP"
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14854. .15132))
/gene="At2g02270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="synonym: T16F16.8; predicted by genscan and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVSVIDENSYWKSGLVIQGIEFRPTKKHQVKKKNCIVNILRFFYCNV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: T16F16.7"
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complement(17280. 17307)
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complement(1734. 17896)
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complement(18077. 18151)
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ement(1867)
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                                                                              ranscriptase"
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YKNDRLLIYSYMENGSLDYWLHERNDGPALLKWKTRLRIAQGAAKGLLYLHEGCDPHI
LHRDIKSSNILLDENFNSHLADFGLARLMSPYETHVSTDLVGTLGYIPPEYGQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVCWPEVRGKISCGMLSKGTHYSVYVVFKTANGRSYGFDLVPVTAGGGGGGGGGGGVGKVATKKS
VYFESGNADSRSATGHYSGISEBEBFVEGERERGMNVGPKERVDGWSEVELGKFYIN
NGGCGDDGSDEIEISIMBTONGNWKSGLIIQGIEIRPERSN"
complement (7966. 9209)
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LVGQESSQRHIYFVGPSDQRRDRETRDVTRPTKRKDGWMEAELGQFFNESGCDVVDTS
ILEIKTPYWKRGLIIQGIEFRPTKSLFYI"
                                                                                                                                                                                                                                    RVLNLSRNFTKDSIPLSIFNLKNLQTLDLSSNDLSGGIPTSINLPALQSFDLSSNKFN
SESBEHGHUNSTQIRVTKLAVNYTGRPRGFCKVLLBLHLCLGNNDLTGNIPBDLFH
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TNGFIGGIPKSLANSPSLNLLNLRNNSLSGRLMLNCTAMIALNSLDLGTNRFNGRLPE
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TTLVLTLNFHGEALPDDSSLHFEKLKVLVVANCRLTGSMPRWLSSSNELQLLDLSWNR
LTGAI PSWIGDFKALFYLDLSNNSFTGEI PKSLTKLESLTSRNI SVNEPSPDFPFMK
                                                                                                                                                                                                                                                                                                                                                                                                                           RNESARALOYNOI FGFPPTI ELGHNNLSGPIWEBFGNLKKLHVFDLKWNALSGSIPSS
LSGWTSLEALDLSNNRLSGSI PVSLQQLSFLSKFSVAYNNLSGVI PSGGGPQTFPNSS
FESNHLCGEHRFPCSEGTESALI KRSRRSRGGDI GWAI GIAFGSVFLLTLLSLIVLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHTSPRDACVVASVSKŠVKSAAQSDLVWEMFLPSEYSSLVLQSANHLSKKEI FLSLAD
NSVLVENGKKSPWVEKASGKKCYMLSAMELTI I WGDSPAYWKWI TVPESKPEKVAELR
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HLEPKPDGWINSSSSTDCCNWTGITCNSNNTGRVIRLELGNKKLSGKLSESLGKLDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRRSGEVDPEIEESESMNRKELGEIGSKLVVLFQSNDKELSYDDLLDSTNSFDQANII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MEQIHGGDSNSGGGGGSSRNDEISVTRASRFDALPEDCISKVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="overlap with BAC clone F504 (AC005936:1. .1865)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="synonym: T16F16.3; pseudogene, phloem-specific
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6867. .72021
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/db_xref="GI:3894158"
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    /rpt_family="AT_rich"
    complement (6000, 7202)
    /gene="At2g02230"
                      complement (<1. .2731)
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note="nore
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gene="At2g02230"
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/gene="At2g02230"
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Complement   Com			ATGICAGGGGGTTTGGGCTTAAATCCAGAAAATGTTCATGTCATATGGGGGAACTCT	TTAAATTGCTAGACATGGCCCATATGTTATAGTAGAATACATTAATAGATAG	ACATATATAAACACAAAGTATCACACTCGACATTCATATACCTTAATTCTGCAGAGA 		CAIGICTICTATTTAAGTTACCCAACATTTTTTGAATAATTTGGCATATATGATTATA 	1381 CCAACATATTATATGGGAACATTTAAAATCTATACGAATGATAACGGTTTATGGAGTAG 1440 	accgaaaaatattatgtatacggaaaatgacaatggatagata	1501 TCTTTCGACTTATATGTCGTCACCATTTGAAACCATAAATTTATAAATTTTCTATGTAT 1560 	1561 ATATATGATATTATGATGTATGCATAAGACAGCTAAACAACAGGGTTGACATAATTATC 1620 	1621 TATGTGTATGTATTGCACATTCACTTGTACTAÀTAAACTAAAATTACGCAATTAAATAT 1680 	1681 ATAAAAATAATAAATATAATCATCTTAATTATATTTGCATTGTTACGTCATATGATAGT 1740 	1741 ACTCTAAATTTCTTCTAAACGIGCTATCTTTTTTGCTAACTTTACATACTTTG 1800 	1801 TGAATCTTCTTTCAAAACCATATCTTCGATAAATGATATTTTCATAGATATTGTTAGTC 1860 	1861 TATATTTGATAATTTGATATATGTATCAAGTCTCTAATCAATGTGCTCATGTATAATTAT 1920
TOUR SESTION OF THE EVERSKOLAR FUNCE PEEBLIKLRS FUNDELLEGUENES  KRULOJARYKKTGDOSCILSECKKKI DESDEKGFLATALALDGEGUIVVDDK  KRULOJARYKKTGDOSCILSECKKKI DESDEKGFLATALALDGEGGILVVDDK  KRULOJARYKKTGDOSCILSECKKKI DESDEKGFLATALALDGEGGILVVDDK  BOB 1970078 118716.9"  TOUR 10.00 10.1016.216822558,2268022798,23088  TOUR 11.00 10.	8 6 8 6 8 6 8	ර සි ර	ት <b>ብ</b> (	රි සි රි	à a	oy Q	රි සි	è 8	è 8	à a	& A	දි සි	& a	යි යි	<b>አ</b>	ð
TOUR SESTION OF THE EVERSKOLAR FUNCE PEEBLIKLRS FUNDELLEGUENES  KRULOJARYKKTGDOSCILSECKKKI DESDEKGFLATALALDGEGUIVVDDK  KRULOJARYKKTGDOSCILSECKKKI DESDEKGFLATALALDGEGGILVVDDK  KRULOJARYKKTGDOSCILSECKKKI DESDEKGFLATALALDGEGGILVVDDK  BOB 1970078 118716.9"  TOUR 10.00 10.1016.216822558,2268022798,23088  TOUR 11.00 10.	÷				•					•					•	
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CR381364 541 bp DNA linear STS 27-MAR-2004
Arabidopsis thaliana transposon insertion STS GT_5.101351, sequence
tagged site.
CR381364.1 GI:45772845
STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a grap dissociation transposon, M a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. 3 denotes a sequence derived from the 3'end of the transposon, GARNet, ATIS project on BESRC GARNet, ATIS project on the seed stock requests: http://nasc.nott.ac.uk/ NASC stock code: N165702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTAGTTTATTTATTTATTTTGGAATTGATTCGATAAGATCAAAAATACTTGTGAATG
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/note="Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 476.2; DB 1.
Pred. No. 1.6e-68;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                1. .534
/standard_name="GT_5.102100"
                                                                                                                                                                                                                /organism="Arabidopsis |
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="AC005312"
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.7%;
Matches 515; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                AGGCTGABATATCATTGTGCCGAGTGTACAAAAGGCCAGGACTAGAAGATCATCGG
                                                                                                                                           TACCACGITCTCTCTCCACAAGACATCATAACCTAAACTCATCGACATCATCCGGTTTAG
                                                                                                                                                                                              CCTTAAGACAACAACAACAATCATCCTCCTCTAATCATTCCGACAACATCTAACA
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                                            TACCACGTTCTCTCTCCACAAGACATCATAACCATAACTCATCGACATCATCCGTTTAG
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Submitted (26-MAR-2004) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
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STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Arabidopsis thaliana transposon
tagged site.
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Langham, S., LeGrys, C.,
Unpublished
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Clarke, J.H.
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AUTHORS
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REFERENCE
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1062 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative NAM protein (At2g02450) mRNA, partial
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                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1062)

Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Haysshizaki,Y., Ishida,J., Lin,J., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nouyen,M., Palm,C.J., Sakurai,T., Satou,M., Shim,P., Southwick,A., Shinozaki,K., Arabidopsis Full Length cDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-MAR-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, G9 94710, UGS.

Street, Albany, G9 94710, UGS.

Street, Albany, G9 94710, UGS.

Collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Pull-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Annotation is based on the January 2002 version of the Arabidopsis genome submitted to Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RFPL CoNNes; Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldemith,A.D., Lee,J.M., Quach,H.L., Torlumi,M., Yu,G., Bowser,L., Chen,H., Miranda,M., Nguyen,M., Palm,C.J., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIB.
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note="This clone is in a modified pBluescript vector
(PLC-1) as a BamH/XhoI insert."
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/mol_type="mRNA"
/db_xref="taxon:3702"
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/protein_id="AAK26018.2"
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                                                                                                                                                                     GI:13430791
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                                                                                                                                                                                                      Submitted (26-MAR-2004) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a defective suppressor mutator transposon. J denotes a sequence derived from the 3'end of the transposon. Genotes a sequence derived from the 5'end of the transposon BERC GARNET, ATIS project On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock code: N165059.
                                                                           Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S.,
Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACTAGITITATITIATITIGGAATIGATITCGATAAGATCAAAATACTIGTGAATG 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCATACACATATATATAAACACACAAGTATCACACTCGACATTCATATACCTTAATTCT 1253
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/note="Unknown"
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Pred. No. 3.5e-68;
0; Mismatches 8; Indels
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    .541
    /standard_name="GT_5.101351"

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/db_xref="taxon:3702"
/clone="AC005312"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1171)
Yamada, K., Chan, M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Bretr, J.R., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                               Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuun, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-007-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA Annotation based on January 2002 version of the Arabidopsis genome submitted to Genbank.
                                FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 1171
/morganism="Arabidopsis tl
/mol_type="mRNA"
/db_xref="texon:3702"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ecotype="Columbia"
/note="This clone is
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                 GI:24030185
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                 /trānslation="LYRYDPWELPAMAAIGEKEWYFYVPRDRKYRNGDRPNRVTTSGY
MATGADMRRSETSRPIGLKKTLYPYSGKAPKGTRTSWINNBYRLPHFTEKYGKAE
ISLCRYVPKREGWEDHFSYPRSIGSTRHHNRNSSTSRLALRQOGHISSSSNHSDNNLNN
NNNINNLEKLSTEYSGDGSTTTTTNSNSDYTIALANQNIYRPWPYDTSNNTLIVSTR
NNDDDDETAIVDDLQRLVNYQISDGATTLMPQTGAALAWNNIPAGTIPNNALWDWNNP
NYDDDRTAIVDFK"
1062
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Pred. No. 4.2e-67;
0; Mismatches 23
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/gene="At2g02450"
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/translation="maivssttsiipmsnovnnnekciedndhrgggeshvonedead
DHDHDMVMpGFRFHPTEEELIEFYLRRKVEGKRFNVELITFLDLYRYDPWELFAMAAI
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KAPKGTRTENIMBYRLPHETTEKYQKAEISLCRYYKRPGEDHESVPRSLSTRHHNH
NSTSTSRLALRQQQHHSSSSNHSDNNLNNNNNINTULEKLSTSYSGDGSTTTTTNSNS
NYTIALANQNIYRPHYDTSINTLIVSTRNHQDDDETAIVDDLQRLVHYQISDGATTT
MPQTQAALAMNNIYRPRYDTSINTLIVSTRNHQDDDETAIVDDLQRLVHYQISDGATTT
MPQTQAALAMNNIPAGTIPNNALWDWMNPIVPDGNRDHYTNIPPK"
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                                                                     evidence=experimental
product="putative NAM (no apical meristem) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1171;
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                                                                                                                                                                                                                                                                                                                                                                                                       /gene="At2g02450"
/note="compared to genomic sequence"
/replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%; Score 467.2; DB 15; ilarity 82.3%; Pred. No. 4.1e-67; Conservative 0; Mismatches 23;
                                                                                                                    /protein_id="AAN41274.1"
/db_xref="GI:24030186"
.. .1140
gene="At2g02450"
                                                                                                                                                                                                                                                                                                                                                   1141. .1171
/gene="At2g02450"
                                                 'codon start=1
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BT000874 1171 bp mRNA linear PLN 16-OCT-2002 Arabidopsis thaliana clone C104984 putative NAM (no apical meristem) protein (At2g02450) mRNA, complete cds.

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STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
     seed stock requests: http://nasc.nott.ac.uk/ NASC stock
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/note="Unknown"
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Pred. No. 2.5e-66;
); Mismatches 16;
                                                                                thaliana
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/standard_name="GT_5,101339"
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Organism="Arabidopsis th

Mol_type="genomic DNA"

/db &ref="texon:3702"

/clone="AC005312"
                                       Location/Qualifiers
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Best Local Similarity 96.2%;
Matches 506; Conservative (
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code: N165049.
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Direct Submission

Submitted (26-MAR-2004) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. 3 denotes a sequence derived from the 3'end of the
transposon, 5 denotes a sequence derived from the 5'end of the
transposon BBSRC GARNEt, ATIS project
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Arabidopsis thaliana transposon insertion STS GT_5.101339, sequence
tagged site.
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
TTCATCCTCCTCTAATCATTCCGACAACAACCTTAACAACAACAACAACAACATCT
                                                                                                                               CGAGAAGCTCTCCACCGAATATTCCGGCGACGCAGCACAACAACAACAACAG
                                                                                                                                                      TCACCAATACTTTCAAATTGCTCAACAGTTTCATCATACTCAACAACAAAATGCTAACGC
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                                                      TICATCCTCCTCAATCATTCCGACAACAACCTTAACAACAACAACAACATCT
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Clarke, J.H.

Direct Submitsion

Submitted (26-MAR-2004) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
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transposon BBSRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: N165877.
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                                                                                                                                                                                                                                                                  stock code NW20'
                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                                                                                                                                                  Length 505;
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                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                               17.5%; Score 456.2; DB 10; ilarity 97.6%; Pred. No. 3.3e-65; Conservative 0; Mismatches 8;
                                                                                                                                                                                                           thaliana"
                                                                                                                                                                                                                                                             /ecotype="Landsberg erecta NASC
/note="Unknown"
                                                                                                                                                                                                                                                                                            1. .505
/standard_name="GT_5.102321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGAAAAATATTATGTATACGGAAAA 1468
                                                                                                                                                                                            1. .505
/organism="Arabidopsis th
/mol_type="genomic DNA"
/db Aref="taxon:3702"
/clone="AC005312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGAAAAAATATCATGTATACGGATAA
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           495;
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Best Local S
Matches 495
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CR381634
LOCUS
DEFINITION
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              TITLE
JOURNAL
    AUTHORS
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CR381634 530 bp DNA linear STS 27-MAR-2004
Arabidopsis thaliana transposon insertion STS GT\_5.101721, sequence tagged site.
CR381634
CR381634.1 GI:45773115

ACCESSION VERSION

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1014
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                                                                                                                                                                                         Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M. Unpublished
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STS; STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                              Submitseion
Submitseion
Submitted (26-MAR-2004) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UJ, UK
AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a g
trap dissociation transposon, Ma a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. 3 denotes a sequence derived from the 3'end of the
transposon, Senotes a sequence derived from the 5'end of the
transposon, Senotes a sequence derived from the 5'end of the
transposon BSRC GARNEt, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1075 GACTAAATGTCAGGGGGTTTGCGCTTAAATCCA-GAAAATGTTCATGTCATATGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 GACTAAATGTCAGGCGCGCTTTGCGCTTAAATCCATAAAAAATGTTCATGTCATATGTGGG
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/note="Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .530
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Pred. No. 7.8e-64;
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/standard_name="GT_5.101721"
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Best Local Similarity 96.8%;
Matches 489; Conservative
                                                                                                                                                                                                                                                                               2 (bases 1 to 530)
Clarke, J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          code: N165391.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CTTTAGTTTCTTTCTTAAATTAACCTAATTAAACAACCTACATATATATCA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                              /clone="LjT35A11"
/clone_lib="LjT library"
/note="TAC clone:TM0869, synonym:Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            £4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 80577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 234; DB 14; Length 8
Pred. No. 4.1e-29;
0; Mismatches 265; Indels
                                                                                                                           estimated length=unknown 1131. 3230 estimated length=unknown 1337. 4436
                                                                                                                                                                                                                                                            'estimated length=unknown
1367. .11466
'estimated_length=unknowp
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estimated_length=unknown
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53644. .53743
/estimated_length=unknown
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   xref="taxon:34305"
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Best Local Similarity 60.1%;
Matches 500; Conservative (
                                                                                                estimated
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                                                                                      Lotus corniculatus var. japonicus chromosome 4 clone LjT35All, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-001-2004) Shusei Sato, Kazusa DNA Research Institute, Department of Plant Gene Research, 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
Pax:81-92-9334)
* NOTE: This is a "working draft" sequence. It currently
* Consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown:
* This record will be updated with the finished sequence.
                                                                                                                                                                      HTG; HTGS_PHASE1.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eutus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                          Kaneko, T., Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Structural Analysis of a Lotus japonicus Genome. XI. Sequence Features and Mapping of Nine hundred twenty-one TAC Clones Unpublished
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f unknown length
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unknown length
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/mol_type="genomic DNA"
/variety="japonicus"
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clone="LjT46D13"
clone lib="LjT library"
'note="TAC clone:TM0525, synonym:Lotus japonicus"

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        /organism="Lotus corniculatus var. japonicus" /organism="lgenomic DNA" /varIety="japonicus"."
        /varIety="japonicus"...

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70988: gap of unknown length
19 88088: contig of 17100 bp in length
9 88188: gap of unknown length
19 91718: contig of 3530 bp in length.
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Submitted (26-007-2004) Shusei Sato, Kazusa DNA Research Institute,

Submitted (26-007-2004) Shusei Sato, Kazusa DNA Research Institute,

Chiba, 292-0818, Japan (E-mail:ssato@kazusa.or.jp,

URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),

Fax:81-438-52-3934)

* NOTE: This is a "working draft' sequence. It currently

* Consists of 24 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* truns of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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36184 TGTTGTTTAATGTTTATTGTTGGATCTGTTATTGAATCTTTAATGAGCTGAGTTGAATCA 36243
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AP007409.1 GI:56805724
HTG; HTGS PHASE1.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph;
Spermatophyta; Maponitophyta; eudicotyledns; core eudicotyled
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Structural Analysis of a Lotus japonicus Genome. XI. Sequence
Features and Mapping of Nine hundred twenty-one TAC Clones
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OY 843 CATGAACGAGTATCGTCTTCGGCACCATGAAACGAGAAGTACCAAAAGGTA 894	t into 433 fragment	Name Begin End	300001 104 400001 105 500001	06 600001 07 700001 08 800001 09 900001	10 1000001 11 1100001 12 1200001 13 1300001		1800001 1900001 2000001 2100001	220001 230001 240001 250001	026 2600001 027 2700001 028 2800001 029 2900001	3000001 3100001 3200001 3300001	AP008207_034 3400001 3510000 AP008207_035 3500001 310000 AP008207_036 3600001 3710000 AP008207_037 3700001 3810000	3800001 3900001 4000001	4100001 4200001 4300001 4400001	5000001 5 5100001 5 5200001 5 5300001 5	տատա	AP008207_058 5800001 5910000 AP008207_059 5900001 6010000 AP008207_060 6000001 6110000
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CGGAGCTGATAGGATGATCGGAGACTTCTCGGCCTATCGGATTAA 784  GGGGCCGACCGATGATCGAGCCGAGCCCCCTCGGCCTATCGGATTAA 784  GGGGCCGACCGGATGATCGAGCCCGAGCCCCCCCCTCGGCCTA 105615  AGTTTTCTACTTCTGATAAGCCCCTAAGGCCTCCCGAGCAGCTCGGATCA 105675  TGTCTTCTACTCCTGCAAGGCCCCCAAGGGGTCCCAGCAGCTCGATCA 105675  TCGTCTTCCGCACCATGAACCGAGAGTACCAAAGGTATAATTCTAC 904	S AP008207 Accession AP008207
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Katayose, Y., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
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Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J.H., Kim, H.I., Eun, M.Y.,
Yano, M., Jiang, J. and Gojobori, T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
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Direct Submission 2010 Takuji Sasaki, National Institute of Submitted (28-FRB-2010) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki, 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7468)

Tel:81-298-38-7441, Fax:81-298-38-7468)
Genes were predicted from the integrated results of the following:
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                               DB 15; Length 110000;
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                                            Query Match 6.4%; Score 167.6; DB 15; Length Best Local Similarity 71.3%; Pred. No. 3.3e-18; Matches 221; Conservative 0; Mismatches 89; Indels
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join(14818. 14996,15784. .15986,17059. .17140,17333. .17397,
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IQTLQNANRHLIGESIGNYTAKELKSLENRLEKGISRIRSKKHELLFSEIEYMOKREA
DLQNENMFLRAKVAEAERAEHDDQQAAEDDEMAPAPAVGGGSSSGTELEALPATFDTR
EYYQPAPPVSMLAAAAAAAAAQYSSDHHQYALHLGYFKVDSGKGGLL"
                                                                                           RNQATPFSDCSLFFGGPVDMSIFLMRTTDDRPIKGFEEVSPGVCFGFRTDLEKASALL.
KSGAVKPEDLNFYVGYSAMDYDQLLSEIDQGYMHVTSCSSGLISDSLATDPSCLWTEI
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complement(14954. 15214)
gane="post-rotation of the complement (14954. 15214)
/gene="post-rotation of the complement (14954. 15214)
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predicted by GlimmerM
                                                                                                                                                             LKLMGGQYAELSQKPKEDGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="P0434C04.7-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0434C04.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <21867. .>22061
/gene="P0434C04.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21867. .22061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOS
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                (http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://opal.biology.gatech.edu/GeneMark/), SplicePredictor
(http://rgp.dna.affrc.go.jp/RiceHbM/), SplicePredictor
(http://ploinformatics.iastate.edu/cgi-bin/gp.cgi), sim4
(http://ploinformatics.iastate.edu/cgi-bin/gp.cgi), sim4
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap2
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap2
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap4
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap4
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap4
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap4
(http://ploinc.gee.psu.edu/html/docs/sin4.html), gap4
(http://ploinc.gee.psu.edu/html/docs/sin4.html
genomic sequence was searched against NCBI NonRedundant Protein database
with BLASTP. ESTS represent the identified CDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
significant homology to any protein name to indicate the homology to any protein name to indicate the homology to sup protein name is classified as a "hypothetical" protein according to IRGSP standard. A gene
by two or more gene prediction programs is classified as a
probable 'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as a
miscellaneous feature of the sequence.
The oriental of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0434C04 clone has an overlap with P0408G07 (DDBJ: AP003379) clone at 5' end and an overlap with B1099D03 (DDBJ: AP003431) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tränslation="MPFVRTLAFPTLANQIEGEIKSRTERDHGEVDLSSPEEAMSRAE
CGGGEEEERCRYRGVRRRWGKWVSEIRVPGTRERLWLGSYATPEAAAVAHDTAVYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGGAGDGGGGGATLNFPERAAATYGGGAAVARLSPRSVQRVASDAGMAADAQLVAARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAPAPAPATAYARPDHCAGATTARHDELARRGMYGAHAHAAGANARTSGERQLVCAEE
ISVDDMEILM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MWALTPNSGGSSCLPARRTPPPLAAAGEAGSLAAGPGRWCSWRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product = "AP2 domain-containing transcription factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="supported by full-length cDNA(s): AK106349"
complement(join(5471. .6148,6846. .6973,7779. .8037))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join(5213. .6148,6846. .6973,7779. .8060))
/gene="P0434C04.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Wipponbare"
/db xref="taxon:39947"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bimilar to Oryza Bativa chromosome 5, P0426G01.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="start and end point are not identified"
oin(2637. .2646,3433. .4109)
gene="P0434C04.1"
GENSCAN (http://ccr-081.mit.edu/GENSCAN.html), PGENESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contains full-length cDNA(s): AK106349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains EST(s): C74866(E60517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oin(<2637. .2646,3433. .>4109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="BAD82116.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="BAD82117.1"
db_xref="GI:56785229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5213. .8060)
/gene="P0434C04.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db xref="GI:56785228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637. .4109
gene="P0434C04.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="P0434C04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="P0434C04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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us-10-780-703-3.rge

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Direct Submitselon

Submitted (31-MAR-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba. Inaraki, 30-8602, Japan

(E-mail:tsasakienias.affrc.go.jp, URLihttp://rgp.dna.affrc.go.jp/,
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(E-mail:tsasakienias.affrc.go.jp/ URLihttp://rgp.dna.affrc.go.jp/,
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.tigr.org/tdb/glamerm/glmr.form.html), FGENESH
(http://rgp.dna.affrc.go.jp/RiceHMA/), SplicePredictor
(http://rgp.dna.affabase an Rgp or DBDJ, Procein donnologies of the coding
regions were searched against NoBl NoRedundant Protein is
SpliceDredictor protein name to indicate the homology Level
such as same name, 'putative-' and '-like protein'. A gene without
slighticant homology to any protein but with full-length of predicted
by two or more gene prediction program is also classified as a probable 'hypothetical' protein according to IRGS standard. A gene
hypothetical' protein according to IRGS standard. A gene
hypothetical protein according to IRGS standard. A gene
hypothetical' protein and selection but with full-selected by a single
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2270. .2482)
/gene="B1099D03.1"
join(492. .854,897. .1173,1427. .1509,1733. .1864,1953. .2025,
2270. .2482)
/gene="B1099D03.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeg.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            this category is not included in IRGSP standard" complement (join(4088. .4327,4393. .4515,4599. .4709,4806. .5046,5273. .5621))
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complement (join(4088. .4327,4393. .4515,4599. .4709,4806. .5046,5275. .5621))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
The genome sequence and structure of rice chromosome 1 Nature 420 (6913), 312-316 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="retroelement-like protein"
complement(3633, .3800)
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                                                                                                                                        Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3633. .3800)
/gene="B1099D03.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted by GlimmerM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="B1099D03"
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                                                                                                          (bases 1 to 191022)
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   TITLE
JOURNAL
PUBMED
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                                                                                                                                                                                TITLE
JOURNAL
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                                                                                                          REFERENCE
                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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Katayose,Y., Wu,J., Niimura,Y., Cheng,Z., Nagamura,Y.,
Antonio,B.A., Kanamori,H., Hosokawa,S., Msukawa,M., Arikawa,K.,
Antonio,B.A., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K.,
Hamada,M., Harada,C., Hijishita,S., Honda,M., Ichikawa,Y.,
Idonuma,A., Iijima,M., Ikeda,M., Iken,M., Ichikawa,Y.,
Ito,Y., Iwabuchi,A., Kamiya,K., Karasawa,W., Katagiri,S.,
Kikuta,A., Kobayashi,N., Komo,I., Machita,K., Machara,T.,
Mizuno,H., Mizubayashi,T., Mukai,Y., Nagasaki,H., Nakashima,M.,
Nakama,Y., Nakamura,M., Namiki,N., Negishi,M.,
Ohta,I., Ono,N., Salji,S., Sakai,K., Shibata,M., Shimokawa,T.,
Shomura,A., Song,J., Takazaki,Y., Terasawa,K., Tsuji,K., Waki,K.,
Yamagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yukawa,K.,
Zhong,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,
Yano,M., Jiang,J. and Gojobori,T.
                                                                                                   non-coding transcript
probably inactive due to 5'UTR too long in CDS"
join (23140, 225674, 24246, 25033. 25178,25498. 25614,
25709. 25825,2659. 26682,26780. 27409)
/gene="P0434C04.7-1"
join (23565. 22574,24261. 24346,25033. 25178,25498. 25614,
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/note="contains EST(8):
D40498 (S2523),AU095566 (R4091),AU033072 (S2523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126237 GGAAGGCGACGGGCCGACCGGATGATCCGAGCGGAGAACAACGCCCCATCGGGCTCA 126296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126297 AGAAGACGCTTGTCTTCTACTCCGGCAAGGCCCCAAGGCGTCCGCAGCAGCTGGATCA 126356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126117 AGCTCGATGGGGGTGCAGCAATGGCGGCGATAGGGGAAAAGGAGTGGTTCTTCTACGTGC 126176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126177 CTCGGGACAGGAAGTACAGGAACGGGACCGGCCGAACCGGGTGACGGCGTCGCGGTCGTCT 126236
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      845 TGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGTATAAATTCTAC 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      665 CAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      725 GGAAAGCCACCGGAGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 AGATATATGTATATGCAGCTATGGCGGCGATAGGAGAAAGAGTGGTACTTCTATGTGC
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                                        /gene="P0434C04.7-2"
/note="contains full-length cDNA(s): AK120493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP003431.2 GI:20804950
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           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MEGGGGGGGGGGGGGGGGGAPYATRTAEEVFRDLRGFRAGM
IKALTDVBKFYKLCDPEKENLCLYGYPNEFWEVTLPAEEVPEIPERALGINFARDG
MNEKDWLALVAVHSDSWLLSYAFYFGAR FGFDREARRELFNMINNLPTIFEVTGARK
KQAKEKTPNSSSKENKPSSKVQSKAESRSKSKIJSAPKOBEGSGDDGGEEEEDHINTL
CGTCGTNDGKDEFWICCDNCEKWYHGKCVKITPARAEHIKQYKCPDCTNKRARA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MAIADLLPLPASSSMSGLASGHWMCLHVPFTVGASVPFAPLIKP
TCVEIATGAFAPERQTICNESSESSGRLHCSLGQI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904
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                          AU082754 (S14363), AU030871 (E60367), AU173000 (E60367), D48242
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                                                                  contains full-length cDNA(s): AK071139, AK058384, AK058498"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53589 AGAAGACGCTTGTCTTACTCCGGCAAGGCCCCCCAAGGCCTCCGCAGCAGCTCGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGTATAAATTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53409 AGCTCGATGGGGGTGCAGCAATGGCGGCGATAGGGGAGAAAGGAGTGGTTCTTCTACGTGC
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                                                                                                                                                                                                                                                                                              complement (22303. .22808)
/gene="B1099D03.11"
complement (join (<22303. .22314,22581. .>22808))
/gene="B1099D03.11"
/note="start and end point are not identified"
complement (join (22303. .22314,22581. .22808))
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                                                                                             /codon_start=1
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/protein id="BAB9530.1"
/db_xref="GI:20804953"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="B1099D03.11"
/note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.4%; Score 167.6; DB 15; Best Local Similarity 71.3%; Pred. No. 2.9e-18; Matches 221; Conservative 0; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="BAD82363.1"
/db_xref="G1:56784342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3920 from Patent W003000898.
AX654050
       note="contains EST(s):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon start=1
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/gene="B1099D03.8"
/noce="start and end point are not identified"
complement(join(11793. .11996,12814. .12985,13083. .13156))
/gene="B1099D03.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MARALLRITRSYCPLSPSPRLPPPLHHRGAAPPLRFRFLSLSSS
SAPSSSAAATANSSDGPGEKGGGGGWDDYLGMSDDBLMGQCEMGTFKASGPGGQHRN
KRESAVRLRHRPTGIIAQLPERAVQCFYSTVASEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MYGSLKRGGGGYMKVAVLEFNKSVRKYPKRGKATTPTPLLKILP
SLSNKYPKRRKITTPTPITFIYYEISKEGKDNNTNVNYYSDIMQQEQFAVAEISRIS
DTKTLMEQNLCNLKKAIKSPSSDNLRRIVALTRRIGELEEDRTLHCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="MAMSASSLFTIFSPFLISLCEAGSGGGRGGGRWRPAKGDAMA
MMAABRSCARAVGKERRAGGGGRSGAHKNQP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="supported by full-length cDNA(s): AK071139"
complement(join(17634. .17909,17981. .18110,20523. .20751,
21600. .21632,21719. .21869))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (17380. .22093)
/gene="B1099D03.10"
complement (join (17380. .17909,17981. .18110,20523. .20751,
21600. .21632,21719. .22093))
/gene="B1099D03.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="probably inactive due to 5'exon missing in CDS probably inactive due to including stop codon(s) in CDS pseudogene, putative gag-pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                       /note="start and end point are not identified"
complement(join(9051. .9104,9202. .9561))
/gene="B1099D03.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note="start and end point are not identified" |
| oin(10369. .10573,10879. .10901)
| dene="B1099D03.7"
                                                                                                                                                                                                                                            //note="gag-pol polyprotein-like"
complement (9051, .9561)
/gene="B1099D03.6"
complement (join(<9051, .9104,9202, .>9561))
                                               .6445))
                                                                                          .6445))
                                                                                                                                                                                                                                                                                                                                                                                                                                      note="contains EST(s): AU032092(R3496)"
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/gene="B1099D03.7"
gene="B1099D03.3"
note="gag-pol polyprotein-like"
complement(join(5630. .5986,6158.
                                                      /gene="B1099D03,4"
complement(join(5630. .5986,6158.
/gene="B1099D03.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="predicted by FGENESH etc."
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                                                                                                                                /note="gag-pol polyprotein-like"
complement (6458. .6835)
/gene="B1099D03.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="BAD82361.1"
/db_xref="GI:56784340"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/produci="hypochetical protein"
/protein_id="BAD82562.1"
/db_xref="GI:56784341"
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/protein_id="BAD82360.1"
/db_xref="G1:56784339"
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/gene="B1099D03.8"
                                                                                                                                                                                              /gene="B1099D03.5"
'note="~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13741. .14601
/gene="B1099D03.9"
13741. .14601
/gene="B1099D03.9"
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Pred. No. 3.7e-17;
0; Mismatches 90; Indels
Patent: WO 03000898-A 3920 03-JAN-2003;
Syngenta Participations AG (CH)
Location/Qualifiers
1. 1212
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/ mol_type="unassigned DNA"
/db_xref="taxon:4530"
                                                                                                                                       Query Match 6.3%;
Best Local Similarity 70.8%;
Matches 218; Conservative
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Search completed: April 6, 2006, 12:58:34 Job time : 12948 secs

Sequence 173486, Sequence 23771, Sequence 100253, Sequence 20520, A Sequence 319, App Sequence 319, App Sequence 101230, Sequence 287, App Sequence 287, App Sequence 287, App Sequence 287, App

81769, A 173486, 10100,

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287, App 2591, Ap 287, App 25359, A 844, App 20659, A

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12858, A 4069, A 6 4969, A 6 4967, App 807, App 807, App 1879, App 11035, Ap 11035, Ap

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Perfect score:

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Sequence:

Scoring table:

Minimum DB Maximum DB

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RESULT 1

US-10-780-703-1

Sequence 1, Application US/10780703

Publication No. US20050034194A1

Sequence 1, Application WS/10780703

Publication No. US20050034194A1

GENERAL INFORMATION:

APPLICANT: Kim, Yun Hee

APPLICANT: Choi, Fun kyung

APPLICANT: Choi, Yun Hee

APPLICANT: Choi, Yang Do

TITLE OF INVENTION: Gene Controlling Flowering Time of Plants and Method for TITLE OF INVENTION: Manipulating Flowering Time of Plant Using the Same

FILE REFERENCE: 012679-105

CURRENT FILING DATE: 2004-02-19

PRIOR FILING DATE: 2004-02-19

PRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0

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US-10-425-115-10100
US-10-425-115-10100
US-10-425-115-103486
US-10-425-195-10523
US-10-424-599-100253
US-10-225-066A-849
US-10-225-066A-287
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OTHER INFORMATION: CDNA of LOX1
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Sequence 87, Appl
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Sequence 115, App
Sequence 3, Appli
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                            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                 OM protein - nucleic search, using frame_plus_p2n model
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US-10-225-066A-115
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Sequence 87, Application US/10225067
; Sequence 87, Application US/10225067
; Publication No. US20040019925A1
; GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: Rechman, Jose Luis
APPLICANT: Rechman, Jose Luis
APPLICANT: Rechman, Robert A.
APPLICANT: Rechman, Robert A.
APPLICANT: Dubell, Amend T.
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Pilorim, Marsha L.
APPLICANT: Polociffe, Oliver
APPLICANT: Becom, Pierre E.
TITLE OF INVENTION: BIOCHEMISTRY-RELATED POLYNUCLEOTIDES AND
FILE REFERENCE: 51442002042
; CURRENT APPLICATION NUBBER: US/10/225,067
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PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
SPIOR FILING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
SOCTWARE: PASCESC FOR WINGOWS VERSION 4.0
SOCTWARE: PASCESC FOR WINGOWS VERSION 4.0
ENGTH: 1144
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ORGANISM: Arabidopsis thaliana
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, LOCATION: (148)...(1392)
US-10-225-067-87
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APPLICANT: Reddie, James
APPLICANT: Reddie, James
APPLICANT: Broun, Pierre E
APPLICANT: Pilgin, Marsha L
APPLICANT: Pilgin, Marsha L
APPLICANT: Dibell III, Arnold T
APPLICANT: Dibell III, Arnold T
APPLICANT: Pileda, Omaira
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374, 780A
CURRENT APPLICATION NUMBER: 09/837, 944
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR PRILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/336, 049
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PELICATION NUMBER: 10/225, 066
PRIOR PLILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR PILING DATE: 2002-08-09
PRIOR PELING DATE: 2003-08
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US-10-374-780A-2475
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Best Local Similarity:
Query Match:
DB:
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GCGATAGGAGAAAGAGTGGTACTTCTATGTGCCAAGAGATCGGAAATATAGAAATGGA 507
                                                                            GATAGACCGAACCGAGTAACGACTTCAGGATATTGGAAAGCCACCGGAGCTGATAAGGATG
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US-10-374-780A-2475
Sequence 2475, Application US/10374780A
Publication No. US20040019927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
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  Length:
Matches:
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APPLICANT: PLUCKLIN, FREUBER,
APPLICANT: JIANG, Cai-Zhong
APPLICANT: CRELMAN, Robert A
APPLICANT: CRELMAN, Robert A
APPLICANT: CRELMAN, Robert A
APPLICANT: PINEDA, Omaira
APPLICANT: PU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YU, Guo-Liang
APPLICANT: YO, Guo-Liang
APPLICANT: YO, Guo-Liang
APPLICANT: YO, Guo-Liang
APPLICANT: YO, Guo-Liang
APPLICANT: YON WIGHER: US, 10/255, 066A
CURRENT APPLICANTION NUMBER: US, 10/325, 066A
CURRENT FILING DATE: 2001-04-18
FRIOR FILING DATE: 2001-08-09
FRIOR APPLICANTION NUMBER: 60/336, 049
FRIOR PILING DATE: 2001-12-05
FRIOR FILING DATE: 2001-12-13
FRIOR FILING DATE: 2001-12-13
FRIOR FILING DATE: 2001-12-13
FRIOR FILING DATE: 2001-12-13
FRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
FRIOR PLIANG DATE: ALAAA
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; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
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ORGANISM: Arabidopsis thaliana
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FEATURE:

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COTHER INPORMATION: genomic DNA of LOV1 gene
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637 TCCACGGGGGGTCGTCGGGGGACCGGCGGCGGCGGCGGCGGCACCGGTACAGGACAAC
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                                                                                   PAT_MRT4530_87286C.1
                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                  COTHER INFORMATION: Clone ID: US-10-437-963-88434
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57.5%
45.7%
39.9%
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Query Match:
NUMBER OF SEQ ID SEQ ID NO 88434 LENGTH: 1433
                                         TYPE: DNA
ORGANISM: Oryza
FEATURE:
                                                                                                                                                                     Percent Similarity
                                                                                                                            Alignment Scores:
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US-10-437-963-88434

Sequence 88434, Application US/10437963

Fublication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brazbazuk, Brad
APPLICANT: Brazbazuk, Brad
APPLICANT: Li Ping:
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14
                                                                                                                            187
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    Conservative:
Mismatches:
Indels:
Gaps:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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 183 GAGCTCATCGACTTCTACCTCCGCCGTAGGGTGGAGGGCAAGCGTTTCAACATCGAGCTC 242
                                IleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuProAlaMetAlaAlaIle 102
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: Las Rosa, Thomas J:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
                                                                                                                                                                                       -GGCAGCTCCGCCGCTGCCATTGATGAGCTGGTGGTGGTGGGCCACGCAGCACGCCGTC 1109
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GCCAAGCCTTGCGGCGCTACCTGCAGAATTCCTCGATGGCTTCCGCTGCCGGCGCGAT 930
                                                                931 CAGCAGCAGCAATTTCAGCAAGACTTCGCGGCGCATTGTACCAGCAGTACTCCAAGAAC 990
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                                                                                                                                                                 pAspAspGluThrAlaIleValAspAspLeuGlnArgLeuValAsnTyr------
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-425-115-10100
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Best Local Similarity:
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ORGANISM: Zea mays
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 ArgProGlyValGluAspHisProSerValProArgSerLeuSerThrArgHisHisAsn
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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737.00
80.0%
73.2%
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US-10-425-115-173486
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
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Pred. No.:
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                                                                                                           APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5)3213)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 81769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 GCCTTCGTCGACCTCTACCGCTATGACCCGTGGGGATCTTCCCGCTCTGGCCTCAATTGGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLysGluTrpTyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArgPro 123
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_81262C.1
US-10-437-963-81769
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LOCATION: (1)..(743)
OTHER INFORMATION: unsure at all n locations
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781.00
89.5$
80.8$
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity:
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US-10-425-115-173486
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 100253
LENGTH: 1902
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               ValGluAspHisProSerValProArgSerLeuSerThrArgHisHisAsnHisAsnSer 220
                                           681 crocadocagadocricoccaarocaagadarocag---adagoarcaagricacogagac 625
                                                                                                                                    234 HisserSerSerSerAsnHisSerAspAsnAsnLeuAsnAsnAsnAsnAsnIleAsnAsn 253
                                                                                                                                                         254 LeuGluLysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThrAsn 273
                                                                                                                                                                                                                              504 GCGCCGTCCGGCAGCAGCAAGAACGGCGCGCTGGCGCACCAAGGAAGCCAAGAAG 445
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                                                                                            -----ArgGlnGlnGlnHis
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Matches:
Conservative:
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         APPLICANT: Cao, Yorgwei
APPLICANT: Cao, Yorgwei
APPLICANT: Buw, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US,10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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Conservative:
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US-10-437-963-53771
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545.00
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37.0%
zhou, Yihua
Cao, Yongwei
Wu, Wei
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Query Match:
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Screen, Steven E
Tabaska, Jack E
                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
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Best Local Similarity:
Query Match:
DB:
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646 TGAGTACCGTGTTACTGAAAACAAGCCTAACAATAGGCCTCCTGGGTGTGACTTGGGCCA
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                                                           sAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProIleGlyLeuLysLy
          gAspArgLysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrT
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Publication No. US20040034888A1
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Zhou, Yihua Kovalic, David K.

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi

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Molecules Associated With It Improvement
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Matches:
Conservative:
Mismatches:
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; OTHER INFORMATION: Clone ID: LIB3242-006-H7_FLI
US-10-425-114-20520
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof fo
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 20520
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Search completed: April
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APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre BIOUN, PIETRE BROUN, PIETRE PITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI0036-2 US
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                           --SerAsnHi 240
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TTCCATCAACGTGGGCCACATGAGTGCGAGGTTTCACCTTTCAAGGATGTCCACGAGCTA 779
                                                                                              CAGTGGTGCATTGTTGGAAAATGACAGAAACACGTTAGAAGGGGTGGTTATAGGGCAATGG
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                         rArgLeuAlaLeuArgGlnGlnGlnHisHisSerSer--
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CURRENT FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-14
                                                                                                                                   uTyrSerGlyAspGlySer-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
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DUBELL, Arrold T
HEARD, Jacqueline E
PILGRIM, Marsha L
JIANG, Cal-Zhong
REUBER, T. Lynne
CREELMAN, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-849
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6, 2006, 12:19:19

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4996997 seqs, 3332346308 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ID Description	ADW23849 Arabidops	ADX17043 Long Vege	ADD30083 ADD30083 Plant yie	ADE31520 Ade31520 Plant vie	ADI44012 Plant tra	ADW23847 Arabidops	ADX17041 Adx17041 Long Vege	ADA70597 Ada70597 Rice gene		ADA71117 Ada71117 Rice gene	A	ADW18167 Adw18167 Pinus rad	ADO62519 Ado62519 Transcrip	ADO62518 ADO62518 Transcrip	ADXS4580 ADXS4580 Plant fu	ABZ13738 Arabidops	ADA68463 Arabidops	AAC36983 Arabidons	からく ついしょうかん
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## ALIGNMENTS

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Long Vegetative phase 1, LOV1, gene, SEQ ID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in
                                                             CTCAACAAAATGCTAACGCAAACGCATTACAATTGGTGGCTGCGGGCGACTACAGCGA
                                                                                                                                  TTCCAAACAATGCTTTGTGGGTATGTGGAATCCAATAGTACCAGAGAAACAGAGATC
TATATCGTCCAATGCCTTACGACACAAGCAACACACATTGATAGTCTCTACGAGAAATC
                           TATCAGATGGAGGTAACATCAATCACCAATACTTTCAAATTGCTCAACAGTTTCATCATA
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                                                                                                                                                                                                                                                                                                                                    ds; transcription factor; transgenic plant; growth rate; senescence;
seed germination rate; plant vigor; seedling vigor.
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Jiang C, Reuber TL, Creelman RA,
                                                                                                                                                                                                                                                                                                                  Plant yield-related polynucleotide clone G962
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2001US-0336049P.
2001US-0338692P.
2002US-00171468.
                                                                                                                                                                                                                                                             ADD30083 standard; cDNA; 1444
                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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P-PSDB; ADD30084.
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19-NOV-2001; 2
11-DEC-2001; 2
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Pilgrim ML, J
Broun PE;
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producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
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Pred. No. 2e-127;
0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                 Sequence 1444 BP; 490 A; 350 C; 246 G; 358 T; 0 U; 0 Other;
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Matches 701; Conservative
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TCACCAATACTTTCAAATTGCTCAACAGTTTCATCATACTCAACAACAAAATGCTAACGC 1208
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                                                                                                                                                                                 CACAAGCAACACACATTGATAGTCTCTACGAGAAATCATCAAGACGATGATGAACTGC
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                               TICATICCICCICTAATCATICGGACAACAACCTTAACAACAACAACAACATCAACAATCT
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                                                                                             ds, gene; transcription factor; transgenic plant; salt stress resistance; osmotic stress resistance; freezing tolerance; drought tolerance; low humidity tolerance; radiation resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a number of isolated cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription darcor polynucleotides and polypeptides are useful in producing transganic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, e.g. aslt stress resistance, cosmotic stress resistance, tolerance to freezing, drought, low humidity tolerance, or radiation resistance. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, i.e. modified desirable traits, e.g. salt stress resistance or tolerance
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G, Broun PE;
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Pred. No. 2e-127;
0; Mismatches 23; Indels
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Jiang C, Ratcliffe O, Pineda O, Yu G,
                                                                                                                                                                                                                                                                                   /product= "transcription factor"
                                                         Plant yield related polynucleotide clone G962
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148. .1392
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2001US-0336049P.
2001US-0338692P.
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Best Local Similarity 96.8%;
Matches 701; Conservative
                     (first entry)
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P-PSDB; ADE31521.
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19-NOV-2001;
                29-JAN-2004
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Dubell AN,
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I polynucleotide encoding a polypeptide controlling the flowering plants, i.e., either delaying or inducing early flowering of the
                      969 TAACTCTGACGTTACCATTGCTCTAGCCAATCAAAACATATATGGTCCAATGCCTTACGA
                                                                                             1029 CACAAGCAACAACACATTGATAGTCTCTACGAGAAATCATCAAGACGATGATGAAAACTGC
                                                                                                                                                                  1149 TCACCAATACTTTCAAATTGCTCAACAGTTTCATCATACTCAACAAAATGCTAACGC
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                                                                                                                                               CATTGTTGACGATCTTCAAAGACTAGTTAACTACCAAATATCAGATGGAGGTAACATCAA
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   2183 TAACTCTGACGTTACCATTGCTCTAGCCAATCAAAACATATATGGTCCAATGCCTTACGA
                                                                        CACAAGCAACAACACATTGATAGTCTCTACGAGAAATCATCAAGACGATGAAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoo SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana LOV1 coding sequence, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lee JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein"
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1. .1140
/*tag= a
/product= "LOV1 prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 1; 25pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flowering; plant; gene; ss.
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P-PSDB; ADW23848.
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                                                                                                                                                                                                                                                       Haake V;
Keddie J, Broun PE;
                                                                                                                                                                                                                                                                                                                                                                               New transgenic plant comprising a recombinant polynucleotide of any or of more than 500 nucleotide sequences, useful in bioinformatic search methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             789 ACATCATAACCATAACTCATCGACATCCCGTTTAGCCTTAAGACAACAACAACACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.4%; Score 687.2; DB 12; Length 1444; Best Local Similarity 96.8%; Pred. No. 2e-127; Matches 701; Conservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1444 BP; 490 A; 350 C; 246 G; 358 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                       i, Jiang C, Heard JE, F), Adam LJ, Reuber TL, Pineda O, Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 2475; 435pp; English.
                                                                                                                                                                                                                                                        Riechmann JL,
                                                                                                                                                                                                                                                                          Ratcliffe O,
Dubell AN, P
JIANG C.
HEARD J E.
HAAKE V.
CREELMAN R A.
RATCLIFFE O.
                                                                                      ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
DUBELL A N.
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P-PSDB; ADI44013.
                                                                                                                                                                                                                  YU G.
                                                                                                                                                                                                                                                                                           Pilgrim ML,
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(RATC/)
(ADAM/)
(REUB/)
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The present invention relates to the novel gene LOV1 (LONG Vegetative phase 1) from Arabidopsis thaliana and its use in controlling flowering time in plants. LOV1 inhibits the flowering stimulating gene AGL20. LOV1 can be used for manipulating flowering time by over-expressing LOV1 to delay flowering, or inhibiting expression of LOV1 to stimulate flowering. LOV1 is also useful for identifying homologous genes in other plants. The present sequence is the LOV1 coding sequence.
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                                                                                                                                                                                                                                                                             522 GTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGCTGAAATATCATTGTGCCG
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                                                                                                                                                                                                            Gaps
                                                                                                                                                              Score 467.2; DB 14; Lengt... --
Pred, No. 1.7e-83;
...mercheg 23; Indels 105;
                                                                                                                                                                                                                                              GTATCAAGTCTCTAATCAATGTGCTCATGTATAATTATAGGCTGAAATATCA
                                                                                                                                        Sequence 1140 BP; 393 A; 272 C; 216 G; 259 T; 0 U; 0 Other;
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                                                                                                                                                                                                          0; Mismatches
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Best Local Similarity 82.3%;
Matches 596; Conservative
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GTATCAAGTCTCTAATCAATGTGCTCATGTATAATTATAGGCTGAAATATCATTGTGCCG 1942
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                                                                                                                                                                                                                                                                                                                                                                            LOV1 polynucleotide encoding a polypeptide controlling the flowering of plants, i.e., either delaying or inducing early flowering of the
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Pred. No. 1.7e-83;
0; Mismatches 23; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1140 BP; 393 A; 272 C; 216 G; 259 T; 0 U; 0 Other;
                   ä
                                                 88.
                                                                                                                                                                                                                                                                                                            Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14;
                                                LOV1, flowering, plant,
                        coding sequence,
                                                                                                                                                                                                                                                                                                            Ahn JH,
                                                                                                                                                                                                                                                                                                            Yoo SY,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID NO 1; 28pp; English.
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                 (UYSE-) UNIV SEOUL NAT IND FOUND
                        Long Vegetative phase 1, LOV1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%;
82.3%;
                                                                                                                                                                                                                                                         20-FEB-2003; 2003KR-00010772.
                                                                                                                                                                                                                              19-FEB-2004; 2004US-00780703
                                                                                                                  1. .1140
/*tag= a
/product= '
                                                 Vegetative phase 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 596; Conservative
                                                                                                                                                                                                                                                                                                              Choi
                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                      WPI; 2005-054880/15.
P-PSDB; ADX17042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                              Lee JS, Kim YH,
                                                                                                                                                                          US2005034194-A1
                                                                                                                                                                                                   10-FEB-2005
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                                                                                                         Key
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881

ADX17041 standard; cDNA; 1140 BP.

ADX17041

RESULT 7
ADX17041
ID ADX1
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a plant used to

tolerance to sequence was

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220 724 280 784 340 844 400 904

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for altering the
an abiotic stress such as cold
                                                                                                                                                                                                         CAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATT
                                                                                                                                                                          CTCGGGACAGGAAGTACAGGAACGGGACCGGCCGAACCGGGTGACGGCGTCGGGTACC
                                                                                                                                                                                                                                                                   GGAAAGCCACCGGAGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGATTAA
                                                                                                                                                                                                                                                                                    GGAAGGCGACGGGGCCGACCGGATGATCCGAGGAACAACAACGCCCCCATCGGGCTCA
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                                                                                                                                                                                                                                                                                                                             AGAAAACCCTAGTTTTCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGGATCA
                                                                                                                                                                                                                                                                                                                                                                                     TGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGTATAAATTCTAC
                                                                                                                                                 <u> AGATATATGTATATGCAGCTATGGCGGCGATAGGAGAAAAGAGTGGTACTTCTATGTGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stress tolerance; transgenic plant; plant; cereal;
                                                                                         Length 1212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice abiotic stress responsive polynucleotide SEQ ID NO:768
                                                           C; 361 G; 185 T; 0 U; 0 Other;
                                                                                    Scorë 164; DB 8; Length 12
Pred. No. 6.2e-23;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goff
useful for conferring resistance to resistance or bacterial, fungal or viral infection. The present illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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N, Ricke
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2001US-0314662P.
2001US-0325277P.
2001US-0332132P.
                                                           Sequence 1212 BP; 245 A; 421
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                                                                                       6.3%;
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                                                                                                     Best Local Similarity 70.8
Matches 218; Conservative
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T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468
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26-SEP-2001; 2
21-NOV-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                involved in plant resistance or response to pathogenic infection. MI comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                             AGCGGCGTTAGCTATGAACATGATTCCTGCAGGAACGATTCCAAACAATGCTTTGTGGGA
                CATTGTTGACGATCTTCAAAGACTAGTTAACTACCAAATATCAGATGGAGGTAACATCAA
                                                                                                                   2363 TCACCAATACTTTCAAATTGCTCAACAGTTTCATCATACTCAACAACAAAATGCTAACGC
                                                                                                                                                                           AAACGCATTACAATTGGTGGCTGCGGCGACTACAGCGACAACGCTAATGCCTCAAACTCA
                                                                                                                                                                                                         ------AGCGACAACGCTAATGCCTCAAACTCA
                                                                                                                                                                                                                                                                 1017 AGCGGCGTTAGCTATGAACATGATTCCTGCAGGAACGATTCCAAACAATGCTTTGTGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method (M1) for identifying genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant; bacterial infection; fungal infection; viral infection; rice;
   CACAAGCAACAACATTGATAGTCTCTACGAGAAATCATCAAGACGATGATGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goff SA, Hou Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; SEQ ID NO 3920; 899pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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pathogenic infection
bacterial, fungal or
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7, Quan S,
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Katagiri F,
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gene;

ADA70597 RESULT

460

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Katagiri

SA,

Claim

gene

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and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polymucleotides. Also disclosed are methods for using the polymucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polymucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polymucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmocic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                     polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1212 BP; 245 A; 421 C; 361 G; 185 T; 0 U; 0 Other;
                        novel abiotic
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ö Length 1212; 90; Indels Score 164; DB 11; Pred. No. 6.2e-23; 0; Mismatches 90; Query Match 6.3%; Best Local Similarity 70.8%;

340 161 AGCTCGATGGGGGTGCAGCAATGGCGGCGATAGGGAGAAGGAGGAGTGGTTCTTCTACGTGC 220 724 CTCGGGACAGGAAGTACAGGAACGGGAACGGCCGAACCGGGTGACGGCGTCGCGTACT 280 GGAAAGCCACCGGAGCTGATAGGATGATCGGAGACTTCTCGGCCTATCGGATTAA 784 844 TGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGTATAAATTCTAC 904 **AGAAAACCCTAGTTTTCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGGATCA** CAAGAGATCGGAAATATAGAAATGGAGATAGACCGAAACCGAGTAACGACTTCAGGATATT GGAAGGCGACGGGCCGACCGGATGATCCGAGCCGAGAACAACCGCCCCATCGGGCTCA 605 AGATATATGTATATGCAGCTATGCCGCGATAGGAGAGAAGAGTGCTACTTCTATGTGC Gaps Matches 218; Conservative TATAACTC 912 221 725 281 785 845 905 665 341 401 a Š g ઠે a ò g ઠે g ઠે

DNA; 1250 BP Plant; bacterial infection; gene; ds. (first entry) Rice gene, SEQ ID 4440. ADA71117 standard; 20-NOV-2003 ADA71117 gene; RESULT 10 ADA71117 EXPXPXPXBXSXFXBXPXPXPXPXPXPXPXPXP

TATGCCGC

461

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fungal infection; viral infection; rice;

WO2003000898-A1 Oryza sativa

22-JUN-2001, 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105

03-JAN-2003

(SYGN ) SYNGENTA PARTICIPATIONS AG.

Υ; Goff SA, Cooper B, Glazebrook J, Chen W, Ä Chang

(SYGN ) SYNGENTA PARTICIPATIONS AG

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                                                                                                                                                                                      The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                     2 2
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                                                               Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 GTACCGAAACGGCGATCGGCCCAACCGAGTGACGCCATCGGGGTACTGGAAGGCCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 GGGGGATAGGATGGTGAAGGGGGGGGGGCGCTCCTATCGGCCTCAAGAAGACGCTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 ATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATTGGAAAGCCACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               738 AGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGATTAAAGAAAACCCTAGT
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Pred. No. 6.2e-20;
Xie
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                                                                                                                                                          Claim 6; SEQ ID NO 4440; 899pp; English
Whitham
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χ,
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illustrate the invention.
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                               WPI; 2003-175290/17.
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                                                                                                                           gene expression.
 Katagiri F,
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Plant; bacterial infection; fungal infection; viral infection; rice; 22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105 (first entry) Rice gene, SEQ ID 3634 WO2003000898-A1. Oryza sativa. 20-NOV-2003 03-JAN-2003 gene; 

ADA70311 standard; DNA; 549

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                                                                                                                                                               Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying agene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accegalogeces acces de constante de contra de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGACCGGATGATCCGCGCGAGAACAGCCGCCCCATCGGCCTCAAGAAGACGCTCGTCT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGGATCATGAACGAGTATCGTC 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTACTCCGGCAAGGCCCCCCAAGGGCGTCCGCAGCAGCTGGATCATGAACGAGTACGCT 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 CAGCTATGGCGGCGATAGGAGAGAAGAGTGGTACTTCTATGTGCCAAGAGATCGGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 CCGCAATGGCGGTGATAGGGGAGAAGAGTGGTTCTTCTACGTGCCGCGGGACCGCGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATTGGAAAGCCACCGGAG
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0
                        Hou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 549;
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                            SA, Hou
Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 549 BP; 103 A; 174 C; 194 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                        Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 132.6; DB 8,
Pred. No. 9.6e-17;
0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                           Claim 6, SEQ ID NO 3634; 899pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%;
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                        Cooper 1
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Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         illustrate the invention.
                        Chen W, Co
', Quan S,
                                                                                                                WPI; 2003-175290/17
                                                                                                                                                                                                                                                            gene expression
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                        Chang H,
Katagiri
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variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably linked to the desired mucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height change, enhanced cold, frost tolerance, enhanced cold, frost tolerance, enhanced cold, frost tolerance, enhanced cold, statch as well as improved taste, starch composition, flower longevity and germination, amongst others.

C Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroms or plant height. This polymucleotide is a plant transcription factor cDNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                          o
                                                                                                                                                                                                                       New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
                                                                                                                                                                                                                                                                                                                                      This invention relates to novel isolated plant nucleic acid molecules,
                                                                                       Connett MB, Emerson SJ, Frost MJ;
Higgins C, Lasham A, Lund ST, Magusin A;
Veerakone S, Westwood C, Gause K, Wood M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTATAGGAATGGAGATCGACCTAACAGAGTTACAAAGTCTGGGTATTGGAAAGCTACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           738 AGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGATTAAAGAAAACCCTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 102; Indels
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                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 1946; 1265pp; English.
               06-JUN-2003; 2003US-0476189P
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Matches 193; Conservative
                                                                                                       Grigor M,
Puthigae S,
                                                                                         ပဲ
                                                                                       Bryant
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                                                                                                                                                               WPI; 2005-075542/08.
P-PSDB; ADW18488.
                                                 (ARBO-) ARBORGEN
                                                                                     Bloksberg LN,
Forster RLS,
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                                                                                                         Forster RLS,
Phillips J,
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WPI; 2004-330163/30.
        WO2004031349-A2
                      Jiang C, Hea
Riechmann JL,
     Glycine max
          15-APR-2004
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CCGAACCGAGTAACGACTTCAGGATATTGGAAAGCCACCGGAGCTGATAGGATGATCAGA 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccaaacagagirciggiatiggaaagccaciggaacigancaaatcatcac
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                      CCCGGATTTAGATTCCATCCTACCGAAGAAGAACTCATAGAGTTTTACCTTCGCCGAAAA
                                                                                                                                                                                                                                   CCTTGGGAACTTCCTGGTAAATATACATTCACATAAACACACATAAATCTCATCTCAAACTA
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                                                                         ccnedaritradaritraticccacreareaeaecritrecarrearaccitreceaae
                                                                                                                              GITGAAGGCAAACGCTITAATGTAGAACTCATCACTTTCCTCGATCTTTATCGCTATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 GACCGCTTAGATCACATTTGTCTTCAATTTCTTGCCATAT----
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proteins (1) and nucleotide sequences (II) (ADOS1534-ADOS378). The

sequences can be used to produce transgenic plants, which overexpress
(II), where the transgenic plant has an altered trait as compared to a
non-transgenic plant or wild-type plant. The transgenic plant comprises
an altered trait selected from increased tolerance to cold,
increased sermination in cold, increased tolerance to cold,
increased tolerance to ownit cased tolerance to cold,
increased tolerance to ownitions, increased tolerance to
to phosphate conditions, increased tolerance to disease, including
ingl disease and particularly Erysiphe, Rusarium and Botryis,
increased tolerance to ownitiple fungal pathogens, increased tolerance to
tungal disease and particularly Erysiphe, Rusarium and Botryis,
increased tolerance to multiple fungal pathogens, increased resistance to
cupphosate, increased sensitivity to AGA, reduced sensitivity to AGA,
increased sensitivity to AGC, altered sugar sensing, increased resistance to
glyphosate, altered diower structure, loss of flower determinacy reduced
fertility, altered shoot meristem development, altered branching pattern,
contered stem morphology, altered vascular tissue structure, reduced
fertility, altered shoot meristem development, altered branching pattern,
altered trichome structure, altered seed sheaf
copical dominance, altered trichome development, altered shed
germination, slow growth, fast growth, altered cell profileration,
altered cell profileration, altered cell expansion, altered shed
germination, slow growth, fast growth, altered cell differentiation,
content, lethality when overexpressed, altered seed shape, increased base deed only content,
death, lethality when overexpressed, altered seed shape, increased lost growth, altered seed seed organical content, altered seed seed organical content, altered seed seed organical content, altered seed protein content, altered seed protein content, altered seed protein content, alter
Plant; transcription factor; transgenic plant; abiotic stress tolerance; osmocitc stress tolerance; cold trolerance; heat tolerance; low nitrogen tolerance; low phosphate tolerance; fungal disease; glyphosate resistance; flowering; fertility; seed development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant polynucleotide encoding transcription factor polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adam LJ, R
Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 824 BP; 254 A; 143 C; 154 G; 272 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred, No. 3.2e-14;
0; Mismatches 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Creelman RA,
Keddie JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratcliffe O, C
V, Dubell AN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                   18-SEP-2002; 2002US-0411837P.
17-DEC-2002; 2002US-0434166P.
24-APR-2003; 2003US-0465809P.
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Best Local Similarity 53.1%;
Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heard JE,
JL, Haake
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816

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789 AACCCTAGTTTTCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGGATCATGAA 848
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ZHOU Y.
KOVALIC D K.
SCREEN S E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pests, for conte
improving yield.
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                                                                                                                                                                                                                                                                                                                             21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inidentified
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                                                                                                                           527
                                                                                                                                                                                                                                                                                  ADX54580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu J,
                                                                                                                                                                                                RESULT 15
ADX54580
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                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                         Contracting the uncleotide sequences (111) Authorists 4700-61/78). The sequences can be used to produce transgenic plants, which overexpress (111), where the transgenic plant has an altered trait as compared to a not-transgenic plant or wild-type plant. The transgenic plant comprises an altered trait selected from increased tolerance to abiotic stress, increased tolerance to obiotic stress, increased tolerance to cold, increased tolerance to cold; increased tolerance to increased tolerance to increased tolerance to multiple fungs by phosphate conditions, increased tolerance to multiple fungs by phosphate conditions, increased tolerance to multiple fungs by the cold sensitivity to ABA, reduced sensitivity altered sensitivity altered sensitivity altered sensitivity altered sensitivity altered sensitivity, altered trichome development, altered trichome development, altered cell trichome structure, altered trichome development, altered cell proliferation, altered cell expansion, altered seed development, altered cell proliferation, altered seed seed ripening, altered seed development, altered cell development, altered seed seed tripening, altered seed development, altered seed tripening, altered seed development, altered seed coloration, altered seed seed tripening, altered seed development, altered seed seed tripening, altered seed seed coloration, altered seed seed tripening, altered seed coloration, altered seed seed tripening, altered seed coloration, altered seed seed colorati
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                                                                                                                                                                                                                                                                polypeptides, useful for producing transgenic plants with advantageous properties compared to a reference plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATCGGAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATTGGAA
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                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel plant transcription factor proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                  Adam LJ, Re
Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 879;
                                                                                                                                                                                                                                           recombinant polynucleotide encoding transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80; Indels
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68.0%; Pred. No. 3.5e-13;
iive 0; Mismatches 80;
                                                                                                                                Jiang C, Heard JE, Ratcliffe O, Creelman RA, Riechmann JL, Haake V, Dubell AN, Keddie JS,
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                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 985; 510pp; English
                                                                                         (MEND-) MENDEL BIOTECHNOLOGY INC.
  18-SEP-2002, 2002US-0411837P.
17-DEC-2002, 2002US-0434166P.
24-APR-2003, 2003US-0465809P.
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                                                                                                                                                                                                  WPI; 2004-330163/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local S
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the livention are also useful for a consisting of a sequence. The recombinant DNA construct is useful for plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway. For conferring increased resistance to plant disease, for producing galactomannan. Inginin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cores condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
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467 Agcacitristricia de proceda de contra de c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADX54580 standard; cDNA; 1297 BP.
                                                                                                                                                                                                                                                                                                                                                                      545
                                                                                                                                                                                            849 CGAGTATCGTCTTCCGCAC 867
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05-NOV-2001; 2001US-00985678
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CC polynucleotide that can be used in the recombinant DNA construct of the \mathbb{C}^{2}
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CC invention.  XX  SQ Sequence 1297 BP; 385 A; 275 C; 308 G; 329 T; 0 U; 0 Other;  Ouery Match  Best Local Similarity 66.4%; Pred. No. 5.6e-13;  Matches 180; Conservative 0; Mismatches 88; Indels 3; Gaps 1;  Matches 180; Conservative 0; Mismatches 88; Indels 3; Gaps 1;  Oy 597 TTAATCATAGATATTCTATATTCTCAGCTAGGGGGGAAAGAGGGGGAACTTTCGGGGGAAAGAGGGGAACTTT 656  Db 12 TAAATTGATTGATTAATTTTTCCAGGTAGGGGAATTTCGGTGAAAGAGGGGAACTTT 71  Oy 657 CTATGGCCAAGAGAATATAGAAATAGGAATAGAACGGATAGGACGAGAACGGGTTC 716								
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23         172.4         6.6         813         6         CD575840         CD575840         UCRPTO1         0           24         171.4         6.6         525         8         DT006901         UVG039B06         CVG20628         10         CVG20628         10         6.5         1         1         CM220628         CVG20628         10         6.5         1         4         813         9         AVA28075         CVG29313         AVA28075         CCD60332         CCD60332 <td< th=""><th>ALIGNMENTS  **RESULT 1  AY201074 LOCUS LOCUS LOCUS DEFINITION AY201074 Arabidopsis thaliana Landsberg DNA linear GSS 03-JAN-2005 Genomic clone GT109.D85.08.02.99.b.507, genomic survey sequence. AY201074 AY201074 VERSION AY201074.1 GI:27897028 KEYWORDS SOURCE Arabidopsis thaliana (thale cress) ORGANISM Arabidopsis thaliana CRGANISM Arabidopsis thaliana CRGANISM Arabidopsis thaliana Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  REFERENCE 1 (bases 1 to 507) MCCOMbie.W. R. and Martiener R. A.  AVENTACRS MAY. B. P., Simorowski, J., Arroyo, JM., Vaughn, M.W., Shen, R.,</th><th>TITLE Arabidopsis genomic sequences flanking Ds enhancer and gene traps in transgenic lines JOURNAL Unpublished (2004)  COMMENT Contact: Martienssen RA  CONTACT: Martienssen RA  Cold Spring Harbor Laboratory  I Bungtown RG, Cold Spring Harbor, NY 11724, USA  Tel: 516 367 8329  Fax: 516 367 8329  Fax: 516 367 8369  Email: martiens@cshl.org  Arabidopsis thaliana sequence flanking Ds5 end of Ds-Trap insertion from line GT109.  Class: transposon-tagged.  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  //mol type='genomic DNA"  //mol type='genomic DNA"  //clone="taxon:3702"  //clone="taxon:3702"  //clone="taxon:3702"  //clone="taxon:3702"</th><th>Query Match Best Local Similarity 98.4%; Pred. No. 1.3e-81; Matches 492; Conservative 0; Mismatches 5; Indels 3; Gaps 2; Qy 457 TCGATCGTTAACAATTCTCAATATCTTTAAACGCTTCTCCCTCTTTAGTTTCTTTAA 516  </th></td<>	ALIGNMENTS  **RESULT 1  AY201074 LOCUS LOCUS LOCUS DEFINITION AY201074 Arabidopsis thaliana Landsberg DNA linear GSS 03-JAN-2005 Genomic clone GT109.D85.08.02.99.b.507, genomic survey sequence. AY201074 AY201074 VERSION AY201074.1 GI:27897028 KEYWORDS SOURCE Arabidopsis thaliana (thale cress) ORGANISM Arabidopsis thaliana CRGANISM Arabidopsis thaliana CRGANISM Arabidopsis thaliana Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  REFERENCE 1 (bases 1 to 507) MCCOMbie.W. R. and Martiener R. A.  AVENTACRS MAY. B. P., Simorowski, J., Arroyo, JM., Vaughn, M.W., Shen, R.,	TITLE Arabidopsis genomic sequences flanking Ds enhancer and gene traps in transgenic lines JOURNAL Unpublished (2004)  COMMENT Contact: Martienssen RA  CONTACT: Martienssen RA  Cold Spring Harbor Laboratory  I Bungtown RG, Cold Spring Harbor, NY 11724, USA  Tel: 516 367 8329  Fax: 516 367 8329  Fax: 516 367 8369  Email: martiens@cshl.org  Arabidopsis thaliana sequence flanking Ds5 end of Ds-Trap insertion from line GT109.  Class: transposon-tagged.  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  Location/Qualifiers  //mol type='genomic DNA"  //mol type='genomic DNA"  //clone="taxon:3702"  //clone="taxon:3702"  //clone="taxon:3702"  //clone="taxon:3702"	Query Match Best Local Similarity 98.4%; Pred. No. 1.3e-81; Matches 492; Conservative 0; Mismatches 5; Indels 3; Gaps 2; Qy 457 TCGATCGTTAACAATTCTCAATATCTTTAAACGCTTCTCCCTCTTTAGTTTCTTTAA 516
GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd.  OM nucleic - nucleic search, using sw model  Run on: April 6, 2006, 09:13:28; Search time 9249 Seconds  (without alignments)  13182.737 Million cell updates/sec  Title: US-10-780-703-3  Perfect score: 2606 Sequence: 1 atggcaattgtatcctccacctaatattccttttaagtaa 2606 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0  Searched: 41078325 seqs, 23393541228 residues  Total number of hits satisfying chosen parameters: 82156650  Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries  Database: EST:* 1: gb_est1:* 2: gb_est2:* 3: gb_est3:* 4: gb_htc:* 5: gb_est4:* 6: gb_est5:* 7: gb_est6:* 8: gb_est5:* 11: gb_gss1:* 10: gb_gss1:* 11: gb_gss3:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.	# Summaries of the total score distribution. Summaries and is derived by analysis of the total score distribution. Summaries S	185.4 7.1 869 10 CZ081915 CZ98191 184.4 7.1 516 3 B1893633 B1893633 183.2 7.0 586 9 CC955522 CC955522 180 6.9 605 10 AGZ23605 AGZ23605 178.2 6.8 623 8 CX527114 CX527114 178.2 6.8 648 1 AW683672 AW683672 178.2 6.8 653 2 BEZ04243 BEZ04243 176.8 6.8 741 7 CO096386 CO096386

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Adaint Lecharny, Unkny-Evry Unkny-Evrk-1050, Alain Lecharny, 40-1bp. Upgadiff).

Definition of the terms used to describe the quality of the clone: The about 220 sequences from the clone collection were sorted according to clones and clustered. If more than one contig was formed, the clone was designated 'Contamination'. The contigs and singletcons were blasted against CDS puls pseudogenes from the TIGRYS annotation, and the resulting AGI code is presented if more than 90 percent identity was found. The sequences were also blasted against all TIGRYS introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for Seganalysis describe the outcome of the evaluation of the CDS detected after palarwise alignment with CDS plus pseudogenes from the TIGRYS introduced as 'intron found'. The remaining terms for Seganalysis describe the outcome of the evaluation of the against all TIGRYS introduce as introduced or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRYS protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over less than 95 percent identity over less than 95 percent identity over less than 95 percent of the sequence; weak similarity: less than 95 percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTP. Note that the collection contains a few clones for which sequencing was the collection contains a few clones of a which sequencing was
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//clone_lib="WPIZ-ADIS-06876, coordinator Javier
paz-Area), a set of transcription factor ORFs was
generated. The ORFs were produced in a decentralized way
in the labs of the participants. Most of the ORFs were
generated by RT-PCR using cDNA from various A. thaliana
tissues as a template. Initially, it was planned to use
yeast recombination to move the ORFs from the cloning
yeast recombination to move the ORFs from the cloning
yeast recombination to move the ORFs from the cloning
yeast recombination to move the ORFs from the cloning
yeast recombination to move the ORFs from the cloning
yeast recombination to move the ORFs from the cloning
yeast recombination at the DNA core facility of the
DNA. For end-sequencing at the DNA core facility of the
MPI of Plant Breeding Research (ADIS; head: Bernd
Weisshaar), the plasmids were re-transformed into
DH5alpha, arrayed into 96-well places and new plasmid bwas prepared. Re-transformation proved to be difficult
because a number of clones displayed poor growth. Data
submission has been handled by Gabipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1883 GIATCAAGICTCTAATCAATGTGCTCATGTATAATTATAGGCTGAAATATCATTGTGCCG 1942
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G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent
Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and
Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the submitted data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 450; DB 8; Length 901;
81.2%; Pred. No. 1.9e-78;
ive 0; Mismatches 30; Indels 105;
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Seg primer: SeLB GTAACATCAGAGATTTTGAGACAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Arabidopsis thaliana"
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Bielefeld University, Institute for Genome Research
Universitaresstrasse 25, D-31394 Sielefeld, Germany
Email: bernd weisshaar@ni-bielefeld.de
AGI: AT2G02450; SegAnalysis: undetermined frame; Translation: no
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sallowski, R., Coupland, G., Martin, C., Angenen, G.C., Baeumlein, H., Mock, H.P., Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Laux, T., Hordsworth, M., Ruberti, T., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J. Recliff, F., Smeekens, S., REGINF, an EU project on functional genomics of transcription factors from Arabidopsis thaliana Comp. Funct. Genomics 3 (2), 102-108 (2002)
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/mol_type="mRNA"
/db_xref="taxon:3702"
/db_xref="taxon:3702"
/clone="101496158"
/clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."
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(bases 1 to 609.

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis genome Res. 15 (4), 487-495 (2005)
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Best Local Similarity 90.6%; Pred. No. 4.8e-75;
Matches 464; Conservative 0; Mismatches 41;
                                                                  thaliana'
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/organism="Arabidopsis
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
I (bases I to 506)
I (bases I to 506)
Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M.; Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Rastury, K., Borillo, C., Carplo, T., Policky, J., Suzuki, G., Argentine, C., Shah, S.,
Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
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Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
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Contact: Chris Town
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                Ouery Match 15.2%; Score 395.8; DB 9; Length 690; Best Local Similarity 80.3%; Pred. No. 1e-67; Matches 561; Conservative 0; Mismatches 107; Indels 31
                                                                                                       Osborn
                                           9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTTTGTGGGATATGTGGAATCCAATAGTACCAGATGG 2569
                                                      Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtcwm@tigr.org
DNA is from a doubled haploid provided by Tom
Class: sheared ends.
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/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="TO1000DH3"

/db_xref="taxon:3712"

/clone="BOGNE16"
                                                                                                                                              Location/Qualifiers
BOGNE16TF
              Contact: Chris Town
TIGR
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BH666975 19-FEB-2002 BOMKP40TR BO_2_3_KB Brassica oleracea genomic clone BOMKF40,
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                                                                                                                                                                                      Brassica oleracea

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bokaryota, Viridiplantae; Streptophyta; Core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (Bases I to 830)

Whole M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,

Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 838;
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12.8%; Score 333; DB 9;
Best Local Similarity 80.1%; Pred. No. 2.7e-55;
Matches 507; Conservative 0; Mismatches 80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Brassica oleracea"
/organism="Brassica oleracea"
/mol trpe="genomic DNA"
/strain="TO1000DH3"
/db xref="taxon:3712"
/clone="BOMKF40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville,
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Location/Qualifiers
                                                            genomic survey sequence
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DR749909.1 GI:71035249
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KEYWORDS
SOURCE
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DR749909
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicotyledons,
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 622)
  GGCCAAATATCTGGTGGAGGTAACATCAATCACCAATACTATCAAATTGCTCAACAGTTT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="plants at various developmental stages from germination to mature seeds" /lab_host="DH108"
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                                                                                                                                                                                                                 AV827617
AV827617 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-17-121 5'
                                      CATCATACTCAACAACAAAATGCTAACGCAAACGCATTACAATTGGTGGCTGCGGGGGACT
                                                                          CATAATCAACAACTACTA - - - - - AACGCAAATGCGTTGCAATCGGTGACGCGACT
                                                                                                              ACAGCGACAACGCTAATGCCTCAAACTCAAGCGGCGTTAGCTATGAACATGATTCCTGCA
                                                                                                                                                 ACAG----CAGCGTTAACGCCTCAAACGCAGGCGACGTTAGCGATGAACATGATCCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
BIST Genomic Sciences Center
Full Royadal, Teulkuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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/note="Site_1: BamH1; Site_2: Sal1; subjected to
dehydration[1, 2, 5, 10, 24 hr) and cold (1, 2,
hr) treatments"
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Pred. No. 2.3e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                   2574 AGAGATCACTATACTAATATTCCTTTTAAGTAA 2606
                                                                                                                                                                                                                                                                                          AAAGATCATTATACTAATATTCCTTTTAGATAA 597
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93.6%; Pred. No. 2...
0; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="RAFL09-17-121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV827617.1 GI:19869677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.6
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AV827617
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DEFINITION
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ORGANISM
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KEYWORDS
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AV827617
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1883 GTATCAAGTCTCTAATCAATGTGCTCATGTATAATTATAGGCTGAAATATCATTGTGCCG 1942

ORIGIN

FEATURES

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2182
2002
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947 bp mRNA linear EST 19-JUL-2005
85-L020254-065-002-E11-SeLA MPIZ-ADIS-065d Arabidopsis thaliana
CDNA clone 002-E11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Data analysis performed in the frame of REGULATORS (Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance), a Trilateral Co-Operation in Plant Genomics between Spain (MCyT), France (GENOPLANTE) and Germany (GABI) coordinated by G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent Thareau (IBP-Orsay UMR8618 CNRS-UPS, thareau-ad-ibp.u-psud.fr) and allain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE, lecharny-ad-ibp.u-psud.fr) Upefinition of the terms used to describe the quality of the clone:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2183 TAACTCTGACGTTACCATTGCTCTAGCCAATCAAAACATATGTCGTCCAATGCCTTACGA 2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engstroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth
                                                                                                                                                                                                                                                                   442
                                                                                                                                                                                                                                                                                                                                                                                                                                                         502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bubaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             formed, the clone was designated 'Contamination'. The contigs and singletons were blasted against CDS plus pseudogenes from the TIGRV5 annotation, and the resulting AGI code is presented if more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davies, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruberti, Smeekons, Somssich, Weissbaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany
Bamil: bernd.weissbaar@uni-bielefeld.de
AGI: AT2002450; SeqAnalysis: undetermined frame; Translation: no
full cds detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parametrin, P. Valencia, A., Costantino, P., Vittorioso, P., Davies, B Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R., Goupland, G., Martin, C., Angenent, G.C., Baeumlein, H., Mock, H.P., Carbonero, P., Colombo, L., Tonelli, C., Engstrien, P., Zabeau, M., Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M., Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J.

REGIA, an EU project on functional genomics of transcription factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2123 CGAGAAGCTCTCCACCGAATATTCCGGCGACGGCAGCACAACAACAACAACAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                            443 TTCATCCTCCTCTAATCATTCCGACAACAACCTTAACAACAACAACAACAACATCAACAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503 GGAGAAGCTCTCCACCGAATATTCCGGCGACGCAGCACAACAACAACGACCACAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAACTCTGACGTTACCATTGCTCTAGCCAATCAAAACATATATCGTCCAATGCCTTACGA
                                                                                 383 ACATCATAACCATAACTCATCGACATCATCCGGTTTAGCCTTAAGACACAACAACAACAA
                                                                                                                                                                                                                                                                                                                                                              TTCATCCTCCTCTAATCATTCCGACAACAACCTTAACAACAACAACAACAACAACAACTCT
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                                                                                                                                                                                 2003 ACATCATAACCATAACTCATCGACATCCATCCCGTTTAGCCTTAAGACAACAACAACACA
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AV440745.1 GI:7611116
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PUBMED
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AV440745
LOCUS
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                                                                                                            임
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than 90 percent identity was found. The sequences were also blasted against all TIGRv5 introns, and matches longer than 50 bp with 95 percent identity are reported as 'intron found'. The remaining terms for Sequnalyais describe the outcome of the evaluation of the CDS detected after pairwise alignment with CDS plus pseudogenes from the TIGRv5 annotation file. The sequences or contigs for which a full CDS with or without STOP codon was detected, a BLASTP against all TIGRv5 protein sequences was performed. Full perfect: 100 percent identity; full good: better than 95 percent identity over less than 95 percent of the sequence; partial good: better than 95 percent identity over less than 95 percent of the sequence; percent identity over less than 95 percent of the sequence; no similarity: no hit from BLASTP. Note that the collection contains a few clones for which sequencing was not successful, which could have simple technical reasons. Obviously, information about these clones is missing in the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="E. coli DHSalpha"
/lab host="E. coli DHSalpha"
/lab host="E. coli DHSalpha"
/lab host="Vectors properties"
/lone lib="MPIZ-ADIS-065d"
/note="Vectors pDONE3-065d"
/note="Vectors pDONE3-065d"
/note="Vectors pDONE3-063d"
/note="Vector pDONE3-063d"
/note="Vector pDONE3-063d"
/note=sted The ORFS were produced in a decentralized way in the labs of the participants. Most of the ORFS were generated by RT-PCR using cDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFS from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1:
/note clones contain 'RGG1 tag1:
/note clones clones contain 'RGG1 tag1:
/note clones contain '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         project, the GATEWAY system became available and finally all ORFs were transferred into GATEWAY vectors. At the end of the REGIA project, the clones were collected as plasmid DNA. For end-sequencing at the DNA core facility of the MPI of Plant Breeding Research (ADIS; head: Bernd Weisshaar), the plasmids were re-transformed into DHSalpha, arrayed into 96-well plates and new plasmid DNA was prepared. Re-transformation proved to be difficult because a number of clones displayed poor growth. Data submission has been handled by GabiPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 947 Std Error: 0.00
Seg primer: SeLA TCGCGTTAACGCTAGCATGGATCTC.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
ecctype="Columbia"
/db_xref="GAB1:1452250"
/db_xref="taxon:3702"
/clone="002-E11"
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Matches 331; Conservative
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 427)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarasu. Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/clone lib="Arabidopsis thaliana above-ground organ two to
six-week old"
  2182
                                                                                                                                                                                                                                                                                                      AV440745 Arabidopsis thaliana above-ground organ two to six-week old Arabidopsis thaliana clone AP208c08_f 3', mRNA sequence.
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                                                                                                     'note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AIGGCAAITGTAICCTCCCACAACAAGCAICAITCCCAIGAGTAACCAAGTCAACAATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 283)
Newman,T., Gebruin,F.J., Green,P., Keegstra,K., Kende,H.,
McIncosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
    GI:2763856
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    R84139.1
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (Bases I to 468)
Asamizu,E., Nakamura; Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="aboveground organs"
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/clone_lib="Arabidopsis thaliana above-ground organ two to
                                                                            AV442690 Arabidopsis thaliana above-ground organ two to six-week old Arabidopsis thaliana clone APZ08c08_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The First Laboratory for Plant Gene Research
Kaubas DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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(hoI"
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Pred. No. 2.3e-47;
0; Mismatches 2; Indels 0;
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ecotype="Columbia"
db_xref="taxon:3702"
clone="APZ08c08_r"
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                                                                                                                                                             AV442690.1 GI:7613105
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Best Local Similarity 99.3%;
Matches 294; Conservative (
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AV442690/c
                                                                                                  DEFINITION
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/organism="Arabidopsis thaliana"
/mol type="mRNA"
/ecotype="Columbia"
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/clone="154014T7"
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/clone="154014T7"
/clone="154014T7"
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/note="Wector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plante half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems; flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2154
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                                                                                    Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
On Jan 9, 1998 this sequence version replaced gi:930573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 283;
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8.8%; Score 229; DB 8;
Best Local Similarity 90.2%; Pred. No. 9.4e-35;
Matches 249; Conservative 0; Mismatches 26;
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                           Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
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Fax: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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BZ028065
LOCUS
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EST 04-AUG-1998

R84139 287 04-AUG-19 16098 Lambda-PRL2 Arabidopsis thaliana CDNA clone 154014T7, mRNA

sequence. R84139

ACCESSION

DEFINITION

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us-10-780-703-3.rst

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/clone_lib="B.oleracea002".
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                                                                                                                          Brassica oleracea
bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                        (bases 1 to 702)
Delehaunty.K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Mash,W., Fabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oef14 row: h column: 08
Seq primer: -21UPpOT forward
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High quality sequence start: 38
High quality sequence stop: 551
Location/Qualifiers
1.702
                                3H999674.1 GI:23547335
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309; Conserv
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         B.oleracea002 Brassica oleracea genomic, genomic survey
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                                                                                                                                                       Brassica oleracea
Brassica oleracea
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:312"
/clone lib="8-olexeea002"
/note="Vector: pOTw13; Whole genome shotgun library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGAACTCATCACTTTCCTCGATCTTTATCGCTATGATCCTTGGGAACTTCCTGGTAAA
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Delehaunty, Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Mash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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Pred. No. 3.5e-34;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
Washington University School of Medicine
Baalis submissions@watson.wustl.edu
Plate: oed90 row: h column: 05
Seq primer: -21UPpOT forward
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/organism="Brassica oleracea"
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High quality sequence stop: 551.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard K. Wilson
                                                                   BZ028065
BZ028065.1 GI:23591339
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illarity 88.0%;
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Matches 272;
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280 bp

AY201073

BH999674 702 bp DNA linear GSS 07-OCT-2002 oef14h08.bl B.oleracea002 Brassica oleracea genomic, genomic survey

sequence.

LOCUS DEFINITION

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1 (bases 1 to 720).
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Nabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oed90 row: h column: 05
Seq primer: -28RPPOT reverse
Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.8%; Score 202.4; DB 983.5%; Pred. No. 1.8e-29;
                                                                                                                                                                                                                                                                                  organism="Brassica oleracea"
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High quality sequence stop: 551
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Matches 269; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATGAAGATGAAGCTGATGATCATGATCATGACATGGTCATGCCCGGATTTAGATTCCA 219
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                                                                                                                     Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                             1 (bases 1 to 280), May, B.P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R., McCombie, W.R. and Martiensen, R.A.
Arabidopsis genomic sequences flanking Ds enhancer and gene traps in transgent lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 TAAATATACATTCACATAA----------AGACACATAAATCATCA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 TAATGTAGAACTCATCACTTTCCTCGATCTTTATCGCTATGATCCTTGGGAACTTCCTGG 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNA"
/cultivar="ecotype Landaberg"
/db_xref="taxon:3702"
/clone="C1109.D53.08.02.99.b.280"
/clone_lib="Arabidopsis thaliana Landsberg DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 214.4; DB 9; Length 280;
Pred. No. 7.2e-32;
0; Mismatches 6; Indels 22
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                                                                                                                                                                                                                                                                                                                                                                                          end
                                                                                                                                                                                                                                                                                Contact: Martienssen RA
Cold Spring Harbor Laboratory
1 Bungrown Rd., Cold Spring Harbor, NY 11724,
15 516 367 8322
Fax: 516 367 8369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTATTTGGAAATCTTAATTTCTATTCATATGTTAAG 369
                                                                                                                                                                                                                                                                                                                                                                  Email: martiens@cshl.org
Arabidopsis thaliana sequence flanking Ds3
from line GT109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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BZO28439.1 GI:23591741
                                                      AY201073.1 GI:27897027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.2%;
Best Local Similarity 89.9%;
Matches 250; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea
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BZ028439/c
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VERSION
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AUTHORS
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asteraids; lamiida; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 869)
Mueller, L.A., Buels, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,
/mol_type="genounic DNA"
/db_xref="taxon:3712"
/dclone lib="B.oleraxeaa002"
/note="Vector: pofw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prepared in Brassica oleracea TO10000H3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CZ981915 869 bp DNA linear GSS 11-AUG-193466 Tomato MboI BAC Library Lycopersicon esculentum genomic clone SL MboI0066A12 3, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCAGGAACGATTCCAAACAATGCTTTGTGGGATATGTGGAATCCAATAGTACCAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2272 CGAGAAATCATCAAGACGATGATGAAACTGCCATTGTTGACGATCTTCAAAGACTAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.2 ACTACCAAATATCAGATGGAG---GTAACATCAATCACCAATACTTTCAAATTGCTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2389 AGTITCATCATACTCAACAACAAAATGCTAACGCAAACGCATTACAATTGGTGGCTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 cractcagggaaggcrccraaaggcaraagagcractggarrargaargaararcgrcr 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        621 AGCTATGGCGCGATAGGAGAGAAAAGGTGGTACTTCTATGTGCCAAGAGATCGGAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               681 TAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATTGGAAAGCCACCGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
Van Eck,J. and Stack,S.
BAC end sequencing from three Solanum lycopersicon libraries
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%; Score 185.4; DB 10; Length 869; Best Local Similarity 74.3%; Pred. No. 4.2e-26; Matches 234; Conservative 0; Mismatches 81; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4081"
/clone="SL Mbof0066A12"
/lab host="E. coli."
/clone lib="Tomato MboI BAC Library"
/note="Vector: pBeloBAC11; Site_1: MboI"
                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
/mol type="genomic DNA"
/cultivar="Heinz 1706"
                                                              Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
Cornell University
251 Emerson Hall, Ithaca, NY 14853, USA
Tel: 607-255-6557
                                                                                                                                                                                                Email: sgn-feedback@sgn.cornell.edu
Plate: 66 row: A column: 12
Seq primer: SP6
Class: BAC ends
High quality sequence start: 25
High quality sequence stop: 696.
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Search completed: April 6, 2006, 13:42:56 Job time : 9253 secs

432 CATTATTCATTCAAA 446

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217 recadadariererereracedadadadaderedretrererederadadaredada 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 AGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGATTAAAGAAACCCTAGT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        618 TGCAGCTATGCCGCCGATAGGAGAAAGAGTGGTACTTCTATGTGCCAAGAGATCGGAA
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Best Local Similarity 64.2%;
Matches 165; Conservative
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LENGTH: 1216
    72.2
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10136.380 Million cell updates/sec
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Sequence 15129, A
Sequence 16536, A
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Sequence 1
Sequence 1
Sequence 7
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                                                                                                                            April 6, 2006, 09:19:16; Search time 457 Seconds
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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9: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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-09-949-016-16536
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
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Sequence 17296, A
Sequence 11973, A
Sequence 13703, A
Sequence 777, App
Sequence 12900, A
Sequence 12412, A
Sequence 12412, A
Sequence 16915, A
                                                                                            Sequence 11934, A
Sequence 14164, A
Sequence 22, Appl
Sequence 13703, A
                                                            Sequence 1038, Ap
Sequence 17067, A
Sequence 16110, A
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                         US-09-949-016-12387
US-09-949-016-12387
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US-09-949-016-1011034
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US-09-949-016-16915
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231129
266293
18773
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251672
251682
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## ALIGNMENTS

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APPLICANT: Broun, Pierre
APPLICANT: Broun, Pierre
APPLICANT: Riccheman, Jose-Luis
APPLICANT: Riccheman, Jose-Luis
APPLICANT: Reddic, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: Adam, Luc
APPLICANT: Adam, Mares
APPLICANT: Tu, Guo-Liang
APPLICANT: Tu, Guo-Liang
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Warsha
APPLICANT: Pilgrim, Warsha
APPLICANT: Pilgrim, Narsha
APPLICANT: Pilgrim, Narsha
APPLICANT: Pilgrim, Narsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Narsha
Sequence 121, Application US/09533029
Patent No. 6664446
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
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US-09-533-029-121
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677

Gaps

9

Length 1216; Indels

Score 97.4; DB 3; Pred. No. 1.9e-11; 0; Mismatches 86;

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APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REPRENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
BARLIER FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09533029 Patent No. 6664446
Application US/09533029
                                                          APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Reddie, James
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Rauciffe, Oliver
APPLICANT: Raccliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 62.7
Matches 160; Conservative
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US-09-533-029-37
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SEQ ID NO 37
LENGTH: 1409
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  ATGTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAG 718
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                                                                                                             391 CTTCTACGCAGGGAAAGCTCCAAAAGGGATTAAGACCAATTGGATAATGCATGAGTATCG 450
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APPLICANT: Samaha, Nagrand
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Tahang, James
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Reuber, Lynne
APPLICANT: NOWBER: US/09/533,029
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT APPLICATION NUMBER: 00/125,814
EARLIER PILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 3
EBNGTH: 1212
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Pred. No. 4.9e-10;
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; Sequence 3, Application US/09533029
; Patent No. 6664446
                                                                                                                                                          858 TCTTCCGCACCATGAAA 874
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddite, James
APPLICANT: Pineda, Omaira
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Best Local Similarity 61.8%;
Matches 162; Conservative
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US-09-533-029-3
                         337
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RESULT 3 US-09-533-029-37

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379 rccrestrrasccrrstarssrsassaaassaarssracricrrcrcccasssaaa
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                                                                                                                                         618 TGCAGCTATGGCGGCGATAGGAGAAAGAGTGGTACTTCTATGTGCCAAGAGATCGGAA
                                                                                                                                                                                                                                                                         678 ATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGATATTGGAAAGCCACCGG
                                                                      9:
3.5%; Score 90.6; DB 3; Length 1409; 62.7%; Pred. No. 5.6e-10; tive 0; Mismatches 89; Indels 6;
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APPLICANT:
APPLICANT:
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us-10-780-703-3.rni

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GIOVANNONI, JAMES
TANKSLEY, STEVEN
PADMANABHAN, VEERARAGAVAN
KUEZINSKY, DIANE
VREBALOV, JULIA
                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09614408 Patent No. 6762347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 59.99
Matches 163; Conservative
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749 TGATCAGATCGGAGACTTCTCGGCCTATCGGATTAAAGAAAACCCTAGTTTTCTACTCTG 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09614408
Sequence 7, Application US/09614408
GENERAL INFORMATION
APPLICANT: TANKSLEY, STEVEN
APPLICANT: TANKSLEY, STEVEN
APPLICANT: TANKSLEY, STEVEN
APPLICANT: NOENSIE, FREDERICK
TITLE OF INVENTION: NOR GENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REPERENCE: TANK: 213
CURRENT APPLICATION NUMBER: US/09/614,408
CURRENT FILING DATE: 2000-07-12
FRIOR APPLICATION NUMBER: 60/143,357
FRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCELIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 CGGCGATAGGAGAGAAAGAGTGGTACTTCTATGTGCCAAGAGATCGGAAATATAGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                      81; Indels
APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MEI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 914
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                                                                                                                                                                                                                                                                                                                                                                         Query Match . 3.4%; Score 88.4; DB 3; Best Local Similarity 64.1%; Pred. No. 1.5e-09; Matches 150; Conservative 0; Mismatches 81
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Best Local Similarity 60.0
Matches 165; Conservative
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US-09-614-408-7
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963 GAACGACAAGCCGGTTTTTACTTCCGGTGGAACACAAAAGGGTTGGGGTAAAAAGGCGC 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 cccacaacacccccrrrrracrrccccrccaacacacaaaaccrrccccraaaaaccrrcc 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GIOVANNONI, JAMES
APPLICANT: TANKSLEY, STEVEN
APPLICANT: TANKSLEY, STEVEN
APPLICANT: VEBALOV, JULIA
APPLICANT: VEBALOV, JULIA
APPLICANT: WORNAILO, TREDERICK
TITLE OF INVENTION: NOR GENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: TAMK: 213
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,357
PRIOR APPLICATION NUMBER: 60/143,357
PRIOR APPLICATION NUMBER: 60/143,257
NUMBER OF SEO ID NOS: 7
SOFTWARE: PATENTIN VOS: 7
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59.9%; Pred. No. 4.3e-09;
tive 0; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                   854 ATCGTCTTCCGCACCATGAAACCGAGAAGTACCAA 888
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR PLING DATE: 2000-04-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER: 06/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER: 05/2012

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 12776

LEAGURE OF THE OFFICE O
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                                                                                                                                                                                                                                             857 GICTICCGCACCATGAAACCGAGAAGTACCAA 888
                                                                                                                                                                                                                                                                                                               460 GAGTIGTAGAAATAAACAAATAACAAGCCA 491
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)....(187169)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776
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       RIN GENE COMPOSITIONS AND METHODS FOR USE THEREOF
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APPLICANT: TANKSLEY, STEVEN
APPLICANT: VEBALOV, JULIA
APPLICANT: VEBALOV, JULIA
APPLICANT: VEBALOV, JULIA
APPLICANT: VEBALOV, STEVEN
TITLE OF INVENTION: NOR GENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: TAMK:213
CURRENT APPLICATION NUMBER: US/09/614,408
FRIOR APPLICATION NUMBER: 60/143,357
PRIOR FILING DATE: 1999-07-12
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1211;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 86.4; DB 3; Length 1. Pred. No. 4.3e-09; 0; Mismatches 106; Indels
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Pred, No. 9.5e-09;
0; Mismatches 107; Indels
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CURRENT APPLICATION NUMBER: US/09/614,981
CURRENT FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1
LENGTH: 1211
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Patent No. 6762347
GENERAL INFORMATION:
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Ouery Match
Best Local Similarity 59.6%;
Matches 162; Conservative (
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Best Local Similarity 59.9%;
Matches 163; Conservative
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SOFTWARE: Patentin Ver. 2.1
   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                               ORGANISM: Tomato US-09-614-981-1
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LENGTH: 1209
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1812 TCAAAACCATATCTTCGATAATGATATTTTTTCATAGATATTGTTAGTCTATATTTGATA 1871
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Patent No. 684486

Patent No. 684486

Patent No. 684486

Patent No. 684486

REBERAL INFORMATION:

APPLICANT: Xie, Qi

APPLICANT: Institute of Molecular Agrobiology, The National U

APPLICANT: Institute of Molecular Agrobiology, The National U

APPLICANT: Institute of Molecular Agrobiology, The National U

TITLE OF INVENTION: INVOLVED IN COTYLEDON AND LATERAL ROOT DEVELOPMENT

FILE REPERENCE: 2248-115

CURRENT APPLICATION NUMBER: US/09/889,926

CURRENT FILING DATE: 2001-08-18

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                             1872 ATTTGATATATGTATCAAGTCTCTAATGAATGTGCTCATGTATAATTATAGGCTGAAATA
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                                                                         CTICIAAACGIGCIAICITITITIGCIAAIGCIAACITIACAIAGITIGIGAAICITCIT
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Pred. No. 5.2e-08;
0; Mismatches 91;
                             1692 TAAATATAATCATCTTAATTATATTTGCATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 61.3%;
Matches 149; Conservative
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; LOCATION: (89)..(1060)
US-09-889-926-1
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US-09-949-016-17145/c
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Batent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
FRIOR PRILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
SOUTHARE: PRESENCE FREST SOUTH ON NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
CTTCTAAACGIGCIAICTTTTTTGCTAATGCTAACTTTACATAGTTTGTGAATCTTCTT 1811
                                                                                                    TCAAAACCATATCTTCGATAAATGATATTTTTCATAGATATTGTTAGTCTATATTTGATA 1871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(191569)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(19156
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Best Local Similarity
Matches 298; Conservat
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... OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters US-09-806-7088-22
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1191 AGATGCATACACATATATATAAACACACAGTATCACACTCGACATTCATATACCTTAAT 1250
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
FILE REPERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR PILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.1%; Score 79.8; DB 3; Length 1
Best Local Similarity 11.1%; Pred. No. 1.1e-07;
Matches 114; Conservative 371; Mismatches 538; Indels
                                                               1837 TATTTTCATAGATATTGTTAGTCTATATTTGATA 1871
                                                                                                                        6117 AGTATATATATATTTTATATTATATATAGTA
                                                                                                                                                                                                                                                                              Sequence 22, Application US/09806708B
Patent No. 6784342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: promoter
                                                                                                                                                                                                                            RESULT 13
US-09-806-708B-22
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                                                                                TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 17145
LENGTH: 30820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 383;
   Application US/09949016
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                                 Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
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Sequence 12378, Application US/09949016 Patent No. 6812339
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US-09-949-016-12378
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITILE OF INVENTION: WORDER: 2000-04-14
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 18773
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                           TITITIGGGCTCTTTCGACTTATATGTCGTCACCATTTGAAACCATAAATTTATAAATT 1550
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                                                       NAYYTHANNWWGCWNNATDTRRTMWKNNNNNNAGTWKNNNNNNAKNASAAKNYAAAAVKA
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; Sequence 14164, Application US/09949016
; Patent No. 6812339
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 12/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
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  Score 77.4; DB 3; Length 1 Pred. No. 1.2e-06; 0; Mismatches 551; Indels
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Query Match
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Matches 476; Conservative
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Search completed: April 6, 2006, 10:48:09 Job time : 459 8ecs

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6, 2006, 09:38:23; Search time 1372 Seconds (without alignments) 15706.996 Million cell updates/sec
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3: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USIOC_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USIOD_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USIOD_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USIOD_PUBCOMB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-425-114-20659	US-10-424-599-75135	US-10-425-114-29695	US-10-424-599-75131	US-10-425-114-14679	US-10-374-780A-2607	US-10-412-699B-879	US-10-495-918-145	US-10-225-066A-807	US-10-374-780A-97	US-10-225-066A-807	US-10-278-536-73	US-10-225-066A-1035	US-10-302-267-177	US-10-225-066A-1035	US-10-412-699B-885	US-10-278-536-1	US-10-302-267-173	US-09-770-149-588	US-09-938-842A-952	US-09-938-842A-952	US-10-495-918-141
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4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	3.9	9.6	3.9	3.9
110.2	109.6	109.6	109.6	108.8	108.6	108.6	108.6	108.6	108.6	108.6	108.6	108.6	108.6	108.6	107.6	107.6	107.6	102.6	102.6	102.6	102.6
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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y GENERAL INCRAFILION

APPLICANT: Kim, Yun Hee

APPLICANT: Choi, Jong Seob

APPLICANT: Choi, Yun Hee

APPLICANT: Choi, Yun Hee

APPLICANT: Choi, Yang Do

APPLICANT: Aln, Ji Hoon

TITLE OF INVENTION: Manipulating Flowering Time of Plant Bame

FILE REFERENCE: 012679-105

CURRENT PILING DATE: 2004-02-19

PRIOR FILING DATE: 2004-02-19

PRIOR FILING DATE: 2003-02-20

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGRAISM: Arabidopsis thaliana

CORANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GAAAAAGGTATAGAAGACAATGATCATAGAGGCGGCCAAGAGAGTCATGTCCAAAATGAA 120
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100.0%; Pred. No. 0;
ive 0; Mismatches
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LOCATION: (1)...(2606)
OTHER INFORMATION: genomic DNA of LOVI gene
Sequence 3, Application US/10780703 Publication No. US20050034194A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 2606; Conservative
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789 ACAICATAACCATAACTCATCGACATCATCCCGTTTAGCCTTAAGACAACAAAAAACACACA 848
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                                                                                                                                                                                                                                                       CGAGAAGCTCTCCACCGAATATTCCGGCGACGCACCACAACAACAACACAG
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APPLICANT: Heard, Jacqueline E.
APPLICANT: Riechman, Jose Luis
APPLICANT: Riechman, Jose Luis
APPLICANT: Riechman, Jose Luis
APPLICANT: Pilgrim, Marsha L.
APPLICANT: Dubell, Arnold T.
APPLICANT: Dubell, Arnold T.
APPLICANT: Pingl, Omaira
APPLICANT: Pingl, Omaira
APPLICANT: Pingl, Omaira
APPLICANT: Pingl, Omaira
APPLICANT: Broun, Pierre E.
APPLICANT: Pingl, Omaira
APPLICANT: Broun, Pierre E.
APPLICANT: Pingl, Omaira
APPLICANT: BIOCHMISTRY-RELATED POLYNUCLEOTIDES AND
TITLE OF INVENTION: BOLYPEPTIBES IN PLANTS
FILE REFERENCE: 514442002042
CURRENT FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
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APPLICANT: PINEDA, Omaira
APPLICANT: TO, Guo-Lians
APPLICANT: BROUN, Pierre E
FILE REPERENCE: MBIO036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
CURRENT APPLICATION NUMBER: 09/837, 44
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR FILING DATE: 2001-12-05
PRIOR PILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,092
PRIOR PILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 00/318,092
PRIOR APPLICATION NUMBER: 00/318,092
PRIOR APPLICATION NUMBER: 00/318,092
PRIOR APPLICATION NUMBER: 00/318,092
PRIOR PILING DATE: 2001-12-05
PRIOR PILING D
2341 TATCAGATGGAGGTAACATCAATCACCAATACTTTCAAATTGCTCAACAGATTTCATCATA 2400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
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HEARD, Jacqueline E
FILGRIM, Marsha L
JIANG, Cai-Zhong
REUBER, T. Lynne
CREELMAN, RODERT A
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; ORGANISM: Arabidopsis thaliana
US-10-225-066A-115
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Matches 701; Conservative
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                                                                                                                                                                 Score 687.2; DB 7; Length 1444;
Pred. No. 1e-124;
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NUMBER OF SEQ ID NOS: 148
SOFTWARE: FRESEQ for Windows Version
SEQ ID NO 877
LENGTH: 1444
                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                 26.4%;
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Matches 701; Conservative
                                                                                       ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)...(1392)
US-10-225-067-87
                                                                                                                                                                               Similarity
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1TILE OF INVENTION POLYNCECOTIDES AND POLYPEPTIDES IN PLANTS
FILE OF INVENTION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/937,944
PRIOR APPLICATION NUMBER: 09/937,944
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-06-09
PRIOR PILING DATE: 2002-08-09
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Pred. No. 1e-124;
0; Mismatches 23; Indels
Sherman, Bradley K
Riechmann, Jose Luis
Jiang, Cai-Zhong
Heard, Jacqueline E
Haake, Volker
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                                                                                                                                          Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
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Dubell III, Arnold
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Keddie, James
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Best Local Similarity 96.8
Matches 701; Conservative
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US-10-374-780A-2475
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US-10-374-780A-2475
; Sequence 2475, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:

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Gaps ö 2062

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APPLICANT: Lee, Jong Seob
APPLICANT: Kim, Yun Hee
APPLICANT: Kim, Yun Hee
APPLICANT: Kim, Yun Hee
APPLICANT: Yoo, So Yeon
APPLICANT: Ahn, Ji Hoon
APPLICANT: Abn, Sene Controlling Flowering Time of Plants and Method for TITLE OF INVENTION: Manipulating Flowering Time of Plant Using the Same FILE REFERENCE: 102679-105
CURRENT APPLICATION NUMBER: US/10/780,703
CURRENT FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: KR 10-2003-10772
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    Matches 701; Conservative
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APPLICANT: ADAM, LUC J
APPLICANT: DUBELL, Arnold T
APPLICANT: PICARIM, Marsha L
APPLICANT: PICARIM, Marsha L
APPLICANT: PICARIM, Marsha L
APPLICANT: PICARIM, Marsha L
APPLICANT: ARUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: REUBER, T. Lynne
APPLICANT: BRUNCH, Pierre E
TITLE OF INVENTION, VIGLA-Related Polymucleotides and Polypeptides in Plants
FILE REPERENCE: MBI0036-2 US
CURRENT APPLICANTION NUMBER: US/810/225,066A
FILE REPERENCE: MBI0036-2 US
CURRENT APPLICATION NUMBER: 09/837,444
FRIOR PILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR PELING DATE: 2001-12-11
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR PLING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR PLING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SEQ ID NO 115
LENGTH: 1444
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TAACTCTGACGTTACCATTGCTCTAGCCAATCAAAACATATATCGTCCAATGCCTTACGA 1028
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                                         CACAAGCAACAACATTGATAGTCTCTACGAGAAATCATCAAGACGATGATGAAACTGC
                                                                       CACAAGCAACAACACATTGATAGTCTCTACGAGAAATCATCAAGACGATGATGAAAACTGC
                                                                                                                              CATTGTTGACGATCTTCAAAGACTAGTTAACTACCAAATATCAGATGGAGGTAACATCAA
                                                                                                                                                                       CATTGTTGACGATCTTCAAAGACTAGTTAACTACCAAATATCAGATGGAGGTAACATCAA
                                                                                                                                                                                                                                                                                                       APACGCATTACAATTGGTGGCTGCGGCGACTACAGCGACAACGCTAATGCCTCAAACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 115, Application US/10225066A Publication No. US20050160493A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIPPE, Oliver
APPLICANT: RIECHMANN, JOSE LUIS
APPLICANT: ADAM, Luc J
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Best Local Similarity
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2542 1328 2602

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1208 2482

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1077 TATGTGGAATCCAATAGTACCAGATGGAAACAGAGATCACTATACTAATATTCCTTTTAA 1136
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                               23; Indels 105;
                                                                                                                                                                                               Query Match 17.9%; Score 467.2; DB 8; Length 1140; Best Local Similarity 82.3%; Pred. No. 1.6e-81; Matches 596; Conservative 0; Mismatches 23; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942 CATTGTTGACGATCTTCAAAGACTAGTTAACTACCAAATATCAGATGG----
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1140
                                                                                              FEATURE:

NAME/KEY: CDS
LOCATION: (1)...(1137)

COTHER INFORMATION: CDNA of LOV1 gene
US-10-780-703-1
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                                                                  TYPE: DNA 'ORGANISM: Arabidopsis thaliana
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RESULT 7 US-10-424-599-121054 ; Sequence 121054, Application US/10424599 ; Publication No. US20040031072Al

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Sequence 88434, Application US/10437963
; Sequence 88434, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharrov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; SEQ ID NOS: 204966
; SEQ ID NOS: 204966
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 09-21 (53233) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ERNGTH: 785
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_87286C.1
US-10-437-963-88434
                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80317C.1
US-10-424-599-121054
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Pred. No. 6.9e-22;
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ORGANISM: Oryza sativa
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Best Local Similarity
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Sequence 101230, Application US/10425115
| Sequence 101230, Application US/10425115
| Publication No. US20040214272A1
| GENERAL InfoRMATION:
| APPLICANT: La Rosa, Thomas J. APPLICANT: Laou, Yihua
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: 191212) B
| CURRENT APPLICANTON NUMBER: US/10/425,115
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 101230
| LENGTH: 390
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                                     CGAGTATCG 857
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                                                                                                                                                                  858 TCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGTATAAATTCTACTAT
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LOCATION: (1)..(390)
OTHER INFORMATION: unsure at all n locations
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                  TTTCTACTCTGGTAAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
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US-10-425-115-101230
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| Sequence 91769, Application US/10437963
| Sequence 91769, Application US/10437963
| Publication No. US20040123343A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J. APPLICANT: Cao, Yihua APPLICANT: Cao, Yongwei APPLICANT: Boukharov, Andrey A. APPLICANT: Buckharov, Andrey A. APPLICANT: Buckharov, Andrey A. APPLICANT: Buckharov, Andrey A. APPLICANT: Li, Ping I TILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53221)B | CURRENT APPLICATION NUMBER: US/10/437,963 | CURRENT FILING DATE: 2003-65-14 | SEQ ID NO 81769 | SEQ ID NOS: 204966 | SEQ ID NO 81769 | SEQ ID NO 81769 | SEQ ID NOS: 204966 | SEQ ID NOS: 204966 | SED ID NO 81769 | 
                                                                                                                        AGCTCGATGGGGGGGAATGGCGGCGATAGGCGAGAAGGAGTGGTTCTTCTACGTGC 346
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90; Indels
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US-10-437-963-81769
0; Mismatches
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OTHER INFORMATION: unsure at all n locations
218; Conservative
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Sequence 22441, Application US/10424599

Sequence 22441, Application WS/10424599

Sublication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
GURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 52441
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526 TICCITCAGGCGACGGACCGCIACCAAAAGGAAATITCTCTITGCAAAGTGIACAAAC 585
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  46 TCTACGTGGGGAAGGCGCCCAAGGGACTCAGGAGCAGCTGGATCATGAACGAGTACGCC
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                                                                             80 TCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGGATCATGAACGAGTATCGTC
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_18368C.1

US-10-424-599-52441
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
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Best Local Similarity 68.0%;
Matches 176; Conservative 0
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongua
APPLICANT: Zhou, Yongua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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Pred. No. 2.8e-17;
0; Mismatches 85,
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US-10-425-115-10100
                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_897C.1
US-10-425-115-173486
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 173486
LENGTH: 792
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Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.2%;
Matches 191; Conservative
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ORGANISM: Zea mays
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FEATURE:
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
APPLICANT: Cac, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 CURRENT FILING DATE: 2003-04-28 SEQ ID NO 29320 LENGTH: 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1286 inaaritrgaitaaritritigcaggraaggcgartritcggrgagaaagagggggggri 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 TTAATCATAGATATATGTATATGCAGCTATGGCGGCGATAGGAGAAAQAAGAGTGGTGGTT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 CTATGTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TTTCAGCCCTAGAGACAGGAAATACCCTAACGGGTCCCGACCAACAGAGTAGCCGGGTC 131
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 1297;
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4.4%; Score 114.2; DB 7; Length 1
Best Local Similarity 66.4%; Pred. No. 4.5e-12;
Matches 180; Conservative 0; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY001F04_FLI
US-10-425-114-29320
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.4%; Score 114.2; DB 7;
Best Local Similarity 66.4%; Pred. No. 4.1e-12;
Matches 180; Conservative 0; Mismatches 88;
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US-10-424-599-75133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 75133, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Glycine max
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ORGANISM: Glycine max
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8979.715 Million cell updates/sec
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1: /SIDS5/ptodata/2/pubpna/USOB NEW PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/USOB NEW PUB.seq:*
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13: /SIDS5/ptodata/2/pubpna/USOB NEW PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-301-480-568794
US-10-301-480-1182203
US-11-096-568A-30705
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US-11-096-568A-6578
US-11-096-568A-31996
US-11-01-086-25
US-11-121-099-65
US-11-096-568A-31561
US-11-096-568A-7102
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US-11-096-568A-22731
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Sequence 568792,
Sequence 1182201,
Sequence 103, App
Sequence 88, Appl
Sequence 7863, Ap
Sequence 1317, App
Sequence 131746, A
Sequence 13133, A
Sequence 1313, A
Sequence 13133, A
Sequence 13133, A
Sequence 13185, Appl
Sequence 13186, Appl
                                                                                                              Sequence Seq
                                                               Sequence
US-10-301-480-1182202

US-10-301-480-121359

US-11-096-568A-29126

US-11-087-099-50

US-11-1087-099-50

US-11-116-881A-790

US-11-121-086-88

US-11-121-086-88

US-11-096-568A-19208

US-10-301-480-568792

US-10-301-480-1182201

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1 US-11-121-086-96
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## ALIGNMENTS

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Sequence 1242, Application US/11172740
; Bequence 1242, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MASCIA, Peter
; APPLICANT: BROWNER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PHENOTYPES
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; TITLE OF INVENTION: DAIRE: 2005-06-30
; TITLE OF ILING DAIRE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
PRIOR PILING DAIRE: 2004-06-30
; PRIOR PILING DAIRE: 2004-06-30
; PRIOR FILING DAIRE: 2004-06-30
; PRIOR FILING DAIRE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ DIN OL 1242
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4.2%; Score 110.4; DB 11; Length 1606;
Best Local Similarity 63.9%; Pred. No. 1.4e-08;
Matches 184; Conservative 0; Mismatches 101; Indels 3;
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CRGANISM: Arabidopsis thaliana
CRGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1666)
CTHER INFORMATION: Ceres CLONE ID no. 38214
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1666)
COCATION: (1)..(1666)
COCATION: (1)..(1666)
COTHER INFORMATION: Also known as Ceres CDNA ID no. 23373803
US-11-172-740-1242
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1060 AAATACTTGTGAATGGACTAAATGTCAGGCGCGTTTGCGCTTAAATCCAGAAAAATGTT 1119
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                                                                                                                                                                                                                                                                                                                                                                                         718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: POULESRY, TIM S.
APPLICANT: NIELSRY, TIM S.
APPLICANT: WIELSRY, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: 00/11/121,086
CURRENT FILING DATE: 2005-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENT OF NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Gaps
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                                                                                                                                                                                                                                                        ñ
                                                                                                                                                                                                            Length 1219;
                                                                                                                                                                                                                                                                                                    599 AATCATAGATATATGTATATGCAGCTATGGCGGCGATAGGAGAAAGA
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Best Local Similarity 47.5%; Pred. No. 6.2e-05;
Matches 503; Conservative 0; Mismatches 533;
                                                                                                                                                                                                            ; DB 11;
1.8e-05;
           LENGTH: 1219
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1219)
COTATION: (1)...(1219)
US-11-096-568A-31996
                                                                                                                                                                                                            Score 90.8; DB
Pred. No. 1.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               839 GGATCATGAACGAGTATCGTCT 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/11121086
Publication No. US20050266459A1
                                                                                                                                                                                                                 Query Match 3.5%;
Best Local Similarity 61.8%;
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: Homo sapiens
US-11-121-086-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 25
LENGTH: 173602
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SEQ ID NO 31996
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 agaargagrarrrrrrrrragccaraagacaagaaarrrccaacagaaccagaacaa 427
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                                                           371 CTTTAGTCCACGAGATCGGAAGTATCCAAACGGAGCAAGACCAAACAGAGCGGGGGACTTC 430
                                                                                                       AGGATATTGGAAAGCCACCGGAGCTGATA---GGATGATCAGATCGGAGACTTCTCGGCC 773
                                                                                                                                                431 AGGTTATTGGAAAGCGACCGGTACAGATAAACCGGTACTTGCTTCCGACGGTAACCAAAA 490
                                                                                                                                                                                            774 TATCGGATTAAAGAAAACCCTAGTTTTCTACTCTGGTAAAGCCCCTAAAGGCACTCGTAC 833
                                                                                                                                                                                                                                      491 GGTGGCCGTGAAGAAGGCACTACTCTTCTACAGTGGTAAACCACCAAAAGGCGTTAAAAG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 ATCGÁGCAACTACAGCTGGTTTTTTGGAAAGCAACTGGAAGAGACAAGTCCATATACCACA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 craariccaagagarirgccargagaaaacccragriricracacrggrggrgcrccrc 547
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                                                                                                                                                                                                                                                                                 834 TAGTIGGATCAIGAACGAGTAICGICTICCGCACCAIGAAACCGAGAA 881
                                                                                                                                                                                                                                                                                                           91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 92.4; DB 11;
Pred. No. 1e-05;
0; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.8
Matches 147; Conservative
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US-11-096-568A-31996
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LENGTH: 1298
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658 226 718

Gaps

9

Length 963;

Score 90; DB 11; Length 96 Pred. No. 2.3e-05; O. Mismatches 105; Indels

286

-----TCGGATTAAAGAAAACCCTAGTTTTCTACTCTGGTAAAGCCCCTAAAGGCACTC 829

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719 GATATTGGAAAGCCACCGGAGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTA--- 775
                                                                                                                                                                                                                                                                                                287 GTTATTGGAAAGCGACTGGTACAGATAAACCGGTGATTTCAACCGGCGGTGGTGGTAGTA 346
                                                                                                                                                                                                                                                                                                                                                                  347 aaaaagreedagraaaaagcreragrerittacagregraaaccacaaaaggagraa 406
                                                                                                                                                                                             659 ATGTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAG
                                                                                                                                                                                                                 227 TCAGTCCAAGAGATGGGAAATATCCCAACGGAGCTAGACCTAACGGAGCTGCGACTTCCG
                                                                                                                                                           167 AATTTGATCCATGGGAACTTCCCGCGAAAGCTTCGTTTGGAGAACAAGAATGGTATTTTT
                                                                                                                           599 AATCATAGATATGTATATGCAGCTATGGCGGCGATAGGAGAAAAAGAGTGGTACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, TIM S.
APPLICANT: NUELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
SPRIOR PILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PALENTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                      407 AATCAGATTGGATTATGCATGAATATCGGTTAACTGATAATAAACC 452
                                                                                                                                                                                                                                                                                                                                                                                                       830 GTACTAGTTGGATCATGAACGAGTATCGTCTTCCGCACCATGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
; ORGANISM: Arabidopsis thaliana US-11-087-099-65
                                                       Query Match
Best Local Similarity 60.1%;
Matches 172; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 171486
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                                                                       Best Local Sim:
Matches 172;
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                                                                                                       1180 CATTAATAGATA----GATGCATACACATATATATAAACACACAAGTATCACACTCGAC 1234
                                                                                                                                                                                                                                               ATGTTCCTGCTCT-TCCTCACATTAATTCATGTCTTCTATTTAAGTTACCCAACATTTTT 1352
                                                                                                                                                                                                                                                                                                                 1353 TGAAATAATTTGGCATATATGAATTATACCAACATATTTATATGCGAACATTTAAAATCT 1412
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17571 AATATAAATCTATAAATATATTTATATATATCTATAATATATAAATCTATAAATATAT 17512
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                                                                                                                                                   356 ATTCATATGT---TAAGATCTTTCTTCTCTTATCACTTTCTCTCTCTATTTCTTTTT
                                                                                                                                                                                       17511 TTATATATATATATATATATAAATCTATAAATATATTTTATATATATATATATATATATATATA
                                                                                                                                                                                                                            413 TTTAACCTATATATGTACCTACCTCCTTATGAAGTATTACTATGTCGATCGTTAACAATT
                                                                                                                                                                                                                                                                                                      533 AACCTACATATATATCATAAGATATACAAATATGTGTTTTTCATAATTAGCTTATGT
                                        47; Gaps
 Length 171486,
                                      Indels
Score 89.8; DB 14;
Pred. No. 7.1e-05;
0; Mismatches 797;
 Query Match
Best Local Similarity 44.8%;
Matches 685; Conservative
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Sequence 65, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450) B EP
CURRENT APPLICATION WHBER: US/11/087,099
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT PILING DATE: 2005-03-22
SEQ ID NOS: 12464
LENGTH: 963

RESULT 5 US-11-087-099-65

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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
FILE REPRENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 5850
                                                                                                                                                                                                                                                                                                                     APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 33561
LENGTH: 1263
                                                                                            16230 TATAATATATATATATATATATATATATACATATAATATATATATATATATATATATATATAT
392
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                                                                                                                                                                            16110 AATATATATATATATTATATTTAAGA 16082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID no. 13603447
                                                                                                                                          1788 TITACATAGITIGIGAATCTTCTTCAAA 1816
                                                                                                                                                                                                                                                  5-11-096-568A-33561
Sequence 33561, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana
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| LOCATION: (1)..(1263)
| OTHER INFORMATION: Ceres Seq.
US-11-096-5688-33561
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US-11-096-568A-5850
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                                                                                                                                                                                                                                                                                                                                             ----AATATACAAATATATATCTATCATA 17001
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                  ATGTTTAATCATAGATATATGTATATGCAGCTATGGCGGCGATAGGAGAAAAAGAGTGGT
                                                                                       ACTTCTATGTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGA
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
FILLE OF INVENTION: Therby
FILLE REFRENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4700
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PELICATION NUMBER: 60/567,570
SOFTWARE: PALENCE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PALENCE: 2004-05-04
NUMBER: PALENCE: PALE
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60.8%; Pred. No. 0.00038;
iive 0; Mismatches 94;
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Pred, No. 0.0012;
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OTHER INFORMATION: Ceres Seq. ID no. 14303479
                                           Sequence 4700, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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Best Local Similarity 48.0%;
Matches 393; Conservative (
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Best Local Similarity 60.8
Matches 155; Conservative
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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Pred. No. 0.00029;
0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 11;
Pred. No. 0.00011;
0; Mismatches 80;
                                                                                                                              NAME/KEY: misc_feature
i LOCATION: (1)..(1396)
corner information: Ceres Seq. ID no. 14312047
US-11-096-5688-5850
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| LOCATION: (1)..[1395]
| THER INDERATION: Ceres Seq. ID no. 15170403
| US-11-096-568A-7102
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ilarity 63.0%;
Conservative
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Best Local Similarity 63.69
Matches 150; Conservative
TYPE: DNA
ORGANISM: Glycine max
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ORGANISM: Glycine max
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Best Local Similarity
Matches 148; Conserv
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TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 61.3%;
Matches 152; Conservative
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Matches 147; Conservative
           TYPE: DNA
GORGANISM: Oryza sativa
US-10-391-414-4
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LENGTH: 1423
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                                                                                       TTAATTCTGCAGAGACATAGTTTTTCTTACAATTTAT-GACATGAATGTTCCTGCT
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; Sequence 4, Application US/10391414
; Publication No. US2005027879941
; GENERAL INFORMATION:
    APPLICANT: SHINOZAKI, Kazuko
; APPLICANT: ITO, Yusuke
; TITLE OF INVENTION: Stress Induced Promoter Derived From Rice:
    FILE REFERENCE: 382.104
; CURRENT APPLICATION NUMBER: US/10/391,414
; CURRENT APPLICATION NUMBER: JP 2002-377316
; PRIOR APPLICATION NUMBER: JP 2002-377316
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 4
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GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 30488
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                                                                                                                           684
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Score 82, DB 8; Length 1423;
Pred. No. 0.00049;
0; Mismatches 90; Indels
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61.8%; Pred. No. 0.0006;
ive 0; Mismatches 88;
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LOCATION: (1). (897);
CTHER INFORMATION: Ceres Seq. ID no. 4961610
US-11-096-568A-30488
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 990
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Length 990;
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Pred. No. 0.00077;
0; Mismatches 369;
                                                                                    Sequence 1182203, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.4
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1182203
                                                   RESULT 15
US-10-301-480-1182203/c
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                                                                            APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT FILING DATE: 2002-11-21
FRIOR APPLICATION NUMBER: US 10/215,598
FRIOR PRICATION NUMBER: US 60/311,695
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 990;
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llarity 47.4%; Pred. No. 0.00077;
Conservative 0; Mismatches 369;
                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 568794
LENGTH: 990
                            Sequence 568794, Application US/10301480 Publication No. US20060057564A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapien
US-10-301-480-568794
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 337;
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ORGANISM:
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Search completed: April 6, 2006, 09:58:15 Job time : 1165 secs

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Run on:

Sequence:

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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptidi TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 1263
                                                                                                                                                                  Sequence 19208, A Sequence 24215, A Sequence 24215, A Sequence 21312, A Sequence 21312, A Sequence 21313, A Sequence 21313, A Sequence 211595, A Sequence 31706, A Sequence 317146, A Sequence 211595, A Sequence 211555, A Sequence 2115555, A Sequence 2115555, A Sequence 2115555, A Sequence 2115555, 
                                         Sequence 65, Appl
Sequence 7863, Ap
Sequence 5850, Ap
Sequence 4, Appli
Sequence 7102, Ap
Sequence 26116, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 241, App
Sequence 28163, P
Sequence 269, App
                                                                                                           Sequence 4,
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115
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1 US-11-096-568A-31996

1 US-11-096-568A-4700

1 US-11-096-568A-7863

1 US-11-096-568A-7863

1 US-11-096-568A-7863

1 US-11-096-568A-1020

1 US-11-096-568A-2213

1 US-11-096-568A-3133

1 US-11-096-568A-3131

1 US-11-096-568A-31384

1 US-11-096-568A-31384

1 US-11-096-568A-31384
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US-11-096-568A-28163
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no. 13603447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33561, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1263)
OTHER INFORMATION: Ceres Seq. ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Arabidopsis thaliana
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        Command line parameters:

-MODEL=frame+p2n.model -DEV=X1h
-O=/abss/ABSSWEB_spool/US10780703/runat_06042006_101351_6632/app_query.fasta_1
-O=/abss/ABSSWEB_spool/US10780703/runat_06042006_101351_6632/app_query.fasta_1
-DB=Published Applications NA_New -OFMT=fastap -SUFFIX=p2n.rnpbn -MINNATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=blosum62
-LOOPCL=0 -LOOPEXT=0 -UNITS=b1ts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cai -LIST=45 -DOCALIGN=200 -THR_NON==crt -HEAPSIZES=500 -MINLEN=0
-MAX_EN=2000000000 -HOST=abss05h
-WAX_EN=2000000000 -HOST=abss05h
-NORT=101351_6632 -NCFU=6 -ICPU=3
-NO WAAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN IIMEOUT=0.5 -DELOPE - DELOPE - DELOPET=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33561, A
Sequence 1242, Ap
                                                                                                                                          April 6, 2006, 10:24:48; Search time 580 Seconds (without alignments) 2614.156 Million cell updates/sec
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1: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

2: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

3: \SIDS5/prodata/2/pubpna/USOF_NEW_PUB.seq:*

4: \SIDS5/prodata/2/pubpna/USOF_NEW_PUB.seq:*

5: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

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8: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

9: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

10: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

11: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*

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13: \SIDS5/prodata/2/pubpna/USOB_NEW_PUB.seq:*
                        GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                     nucleic search, using frame_plus_p2n model
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US-11-172-740-1242
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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2034
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Match Length DB
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1606
                                           Copyright
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Searched:

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GTTTATGTCGAATATACAAAAGCAAACGAAAGCGCACAAAAAACAAGCTTACAATATCTA
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                                                                   LeuSerThr----ArgHisHisAsnHisAsnSerSerThrSerSer------
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                                                        ProGlyPheArgPheHisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLys
                                                                                               73 ValGluGlyLysArgPheAsnValGluLeuIleThrPheLeuAspLeuTyrArgTyrAsp
                                                                                                                                     ProTrpGluLeuProAlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyrValPro
9 2 4
                                       US-10-780-703-2 (1-379) x US-11-096-568A-33561 (1-1263)
Mismatches:
Indels:
Gaps:
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Sequence 1242, Application US/11172740
Publication No. US20060057724A1
GENERAL INPORMATION:
APPLICANT: MASCIA, Peter
APPLICANT: ALEXANDROV, Nickolai

US-11-172-740-1242

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ENCODED THEREBY USEFUL FO
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APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLECTIDE SEQUENCES AND POLYPEPTIDES ENCY
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
FILE REFERENCE: 2750-1602PUS2
CURRENT APPLICATION NUMBER: US/11/172,740
CURRENT FILING DATE: 2006-06-30
PRIOR APPLICATION NUMBER: 60/583,621
PRIOR PILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR FILING DATE: 2004-06-30
PRIOR PLING DATE: 2004-06-30
PRIOR PLING DATE: 2004-06-30
PRIOR PLING DATE: 2004-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/584,800
PRIOR APPLICATION NUMBER: 50/584,800
PRIOR APPLICATION 1008: 2523
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Mismatches:
Indels:
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Matches:
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LOCATION: (1)...(1606)
OTHER INFORMATION: Also known as
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ORGANISM: Arabidopsis thaliana
FRATURE:
NAME/KEY: misc_feature
LOCATION: (1)._(1606)
OTHER INFORMATION: Ceres CLONE I
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4700
LENGTH: 1191
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NAME/KEY: misc_feature
LOCATION: (1) - (1191)
OTHER INFORMATION: Ceres Seq. ID
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| SUBJECT OF STATE OF THE STATE OF THE
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                         -----ThrArgHisHisAsnHisAsnSerSerThrSerSerArgLeuAlaLeu 228
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CTHER INFORMATION: Ceres Seq. ID
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                                                                                                                            APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Pla
FILE REFERENCE: 38-21(53450) B.P.
CURRENT APPLICATION UNMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 65
LENGTH: 963
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                                                                 Sequence 65, Application US/11087099 Publication No. US20060041961A1 GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-11-087-099-65
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                                              ProglyPheArgPheHisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLys
                                                                                                                                            73 ValGluGlyLysArgPheAsnValGluLeuIleThrPheLeuAspLeuTyrArgTyrAsp
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DNA Fragments and Corresponding Polypeptid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 nGluTyrArgLeuProHisHisGluThrGluLysTyrGlnLysAlaGluIleSer----
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.Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
i LOCATION: (1)...(1396)
i OTHER INFRAMATION: Ceres Seq. ID no. 14312047
US-11-096-568A-5850
                                                                                                   APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNJ
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-15925USZ
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 5850
                                                        Sequence 5850, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            1.41e-39
478.00
50.1%
34.2%
23.5%
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                    APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE OF INVENTION: Therby
FILE OF INVENTION: Therby
FILE SPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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Matches:
Conservative:
Mismatches:
Indels:
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LOCATION: (1). (1). (1304)
OTHER INFORMATION: Ceres Seq. ID no. 15176333
             Sequence 7863, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
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479.50
59.1%
45.0%
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max
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Best Local Similarity:
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Sequence 7102, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
APPLICANTON: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
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                                                                                                                               GlyAspargProAsnArgValThrSerGlyTyrTrpLysAlaThrGlyAlaAspArg 139
                                                                 AlaalaileglyglulysglufrpflyrPheffyrValProArgAspArgLysflyrArgAsn 119
                                                                                                                                                                343 egercececceahocececececececreserresaheseaheseaheseekeeseeceeceana 402
                                                                                                                                                                                              140 MetileArgSerGluThrSerArgProlleGlyLeuLysLysThrLeuValPheTyrSer 159
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                                                                                                                                                                                                                                                                                                                                     517 GICGACCGCTCCGCCAGGAGAACAGCTCAGGTIGGATGATTGGGTGCTGTGCCGG
ValGluLeuileThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuProAlaMet
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Matches:
Conservative:
Mismatches:
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COTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-7102
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473.50
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NAME/KEY: misc_feature
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Best Local Similarity:
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US-11-096-568A-7102
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APPLICANT: KATSURA, Koji
APPLICANT: KATSURA, Koji
APPLICANT: ITO, Yusuko
TITLE OF INVENTION: Stress Induced Promoter Derived From Rice
FILE REFERENCE: 382.1041
CURRENT APPLICATION NUMBER: US/10/391,414
CURRENT FILING DATE: 2003-03-18
PRIOR APPLICATION NUMBER: JP 2002-377316
PRIOR FILING DATE: 2002-12-26
                                                                                                                                                                                                                                                                                                                          859 GAGCGACCCCAAGTGGAACGATGATCTGGACCTAAAGCTAGAAAC----
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SOFTWARE: Patentin Ver.
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ORGANISM: Oryza sativa
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LENGTH: 1423
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LOCATION: (1)..(1189)
OTHER INFORMATION: Ceres
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Best Local Similarity:
Query Match:
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US-11-096-568A-26116
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| GAGCGAGCCAAAGTGGAAAGGTGGGAAAAAGCCTCGAGTTTCGTTTAATTACGTGGA
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TITLE OF INVENTION: Sequence-Determined DNA F.
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2;
CURRENT APPLICATION NUMBER: US/11/096,568A;
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26116
; LENGTH: 1189
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APPLICANT: Abad, Mark S. et al.
TILE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38 2-21 (53450) B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
LENGTH: 1218
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Matches:
Conservative:
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CORGANISM: Glycine max
US-11-087-099-50
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Best Local Similarity:
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPRENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 19208
LENGTH: 1409
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                                   889 ATATGTAAAGCGAAGCCCACGCTCACAGTCGTCGGCCC 927
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          ValThrileAlaLeuAlaAsnGlnAsnIleTyrArgPro
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; Sequence 19208, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
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ORCANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1).(11409)
GTHER INFORMATION: Ceres Seq. ID
US-11.096-568A-19208
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Sequence 22731, Application US/11096568A
Sequence 22731, Application US/2006048240A1
Sequence 22731, Application Wo. US2006048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
LENGTH: 1393
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                                                                                                        778
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                                                                           221
                                                                                                                                       222 ThrSerSerArgLeuAlaLeuArgGlnGlnGlnHisHisSerSerSerSerAsnHisSer 241
                                                                                                                                                                                                   242 AspAsnAsnLeuAsnAsnAsnAsnAsnIleAsnAsnLeuGluLysLeuSerThrGluTyr 261
             sArgValTyrLysArgProGlyVal 201
                                                                                                                                                                   779 AACGATITCCAGTIGTCGTCGTCGGAGCATGAGCACGAGCAGGAGGAGCCGGCGGCG
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OTHER INFORMATION: Ceres Seq. ID no. 12409839
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775 TTATCTGAGAATCATACCAACCACCCACCCAGGGGTTGGATCAAGTGCTGGATTCAACACT 834
                           252 AsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThr 271
                                                          GGGAATITIGGATCAGCAATGCTCTCCAATCAATAACAACCACCTACCAATAATTACATG 894
                                                                                                           TrpTyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgVal 126
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LeuSerThrArgHisHisAsnHisAsnSerSerThrSerSerArgLeuAlaLeuArgGln 230
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                                                                                                                                                                                        IleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGlnLysAlaGluIle 190
                                                                                                                                                                                                                                                                                                                                            GlnGlnHisHisSerSerSerAsnHisSerAspAsnAsnLeuAsnAsnAsnAsn 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       613 TCATCAGAGCTAACTCAAGGGGTCCTTTTAGACGAAGCAAACAGCTCATCCATATTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...----AsnAsnThrLeuIleValSerThrArgAsnHis
                                                                                                    SerLeuCysArgValTyrLysArgProGlyValGluAspHisProSerValProArgSer
                                                                                                                                                                                                                                                       111 ValProArgAspArgLysTyrArgAsnGlyAspArgProAspArgValThrThrSerGly
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526 GAAGAAGAAAAAAGAAGAAGAAGTGGAAAAATGTGATGGTAATTATATTGAAGACGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                      TyrTrpLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProlleGly
                                                                                                                                                                                                                                                                                                                   AAAGGGGAAGAAGAAGAAGCAGAAGAAGAGAGCACTAGT-----GTAGGAAAAGAAGAG
                                                           193 AGCACAÁGGÁTAAGAÁGTÁTCCAAÁTGGĆTCTÁGGACGAÁCCGTGCGACCGAGCGGGT
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Job time : 588 secs
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 30488
LENGTH: 897
                                                                                                   112
                                                                                                                                                  oArgAspArgLysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrTr 132
                                                                                                                                                                                                     pLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProIleGlyLeuLy 152
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                 232 CCCATGGCAGCTCCCAAGGATGGCGCTGTACGGCGAGAAGGAGGGGGTACTTCTTCTCTCCCC 291
                                                                                                                                                                  GCGGGACCGCAAGTACCCGAACGGGTCCAGGCCCAACCGCGCCGCCGGGGCTGGGTACTG 351
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                                                  sValGluGlyLysArgPheAsnValGluLeuIleThrPheLeuAspLeuTyrArgTyrAs 92
   ProGlyPheArg-PheHisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLy
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Conservative:
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ORGANISM: Arabidopsis thaliana
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April 6, 2006, 09:58:27; Search time 239 Seconds (without alignments) 2818.811 Million cell updates/sec
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Sequence 73,
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GenCore version 5.1.7
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/ cgn2 6/ptodata/1/ina/5 COMB.seq:*
/ cgn2 6/ptodata/1/ina/6 COMB.seq:*
/ cgn2 6/ptodata/1/ina/6 COMB.seq:*
/ cgn2 6/ptodata/1/ina/H COMB.seq:*
/ cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
/ cgn2 6/ptodata/1/ina/PCOMB.seq:*
/ cgn2 6/ptodata/1/ina/PP COMB.seq:*
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                                                                         OM protein - nucleic search, using frame_plus_p2n model
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US-09-614-408-1
US-09-614-981-1
US-09-533-029-3
US-09-533-029-37
US-09-533-029-121
US-09-889-926-1
US-09-533-029-73
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
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## ALIGNMENTS

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(BTHC).	o
UUT II 09-614-408-6 equence 6, Application US/09614408 atent No. 6752347 ENERAL INFORMATION: APPLICANT: TANKSLEY, STEVEN APPLICANT: TANKSLEY, STEVEN APPLICANT: WEBALOW, JULIA APPLICANT: NOR GENE COMPOSITIONS AND METHODS FOR USE FILE REFERENCE: TAMK:213 CURRENT APPLICATION NUMBER: US/09/614,408 CURRENT FILING DATE: 1999-07-12 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PARENTIN VET: 2.1 SOFTWARE: PARENTIN VET: 2.1 SOFTWARE: PARENTIN VET: 2.1 SOFTWARE: PARENTIN VET: 2.1 CORGANISM: TOMACO ONCRANISM: TOMACO	Length: Matches: Conservative: Mismatches: Indels: Gaps:
80 80	Length: Matches: Conserva Mismatch Indels: Gaps:
TIO 14,4	Lengt Match Conse Misma Indel Gaps:
10-514-408-6 09-514-408-6 09-514-408-6 equence 6, Application US/09614408 equence 6, Application US/09614408 extent No. 5762347 APPLICANT: GIOVANNONI, JAMES APPLICANT: TANKSLEY, STEVEN APPLICANT: WREBALOV, JULIA APPLICANT: NOR GENE COMPOSITIONS FILLE REFERENCE: TAMK:213 CURRENT APPLICATION NUMBER: US/09/614,408 CURRENT PILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: 60/143,357 PRIOR FILING DATE: 1999-07-12 NUMBER OF SEQ ID NOS: 7 LIENGTH: 1209 LENGTH: 1209 LENGTH: 1209 TYPE: DNA ORGANISM: TOMATO ORGANISM: TOMATO	
ULT 1  APPLICATE OF (572347  APPLICANT: GIOVANNONI, JAMES  APPLICANT: TANKSLEY, STEVEN  APPLICANT: TANKSLEY, STEVEN  APPLICANT: TONESIE, FREDERICK  ITLE OF INVENTION: NOR GENE CON  TITLE OF INVENTION: NOR GENE CON  TITLE REPERENCE: TANK:213  CURRENT APPLICATION NUMBER: US/0  CURRENT FILING DATE: 1999-07-12  NUMBER OF SEQ ID NOS: 7  SOFTWARE: PATENTING VET: 2.1  EQ ID NO 6  LENGTH: 1209  LENGTH: 1209  TTYPE: DNA  ORGANISM: TOMATO  O	8
pplication US/0961 62347 MATION: JAMES IOVANNONI, JAMES IOVANNONI, JAMES TANKSLEY, STEVEN VREBALOV, JULIA NOENSIE, FREDERICK ENTION: NOR GENE C CE: TAMK:213 ICATION NUMBER: US NG DATE: 2000-07- ATION NUMBER: 60/1 DATE: 1999-07-12 Q ID NOS: 7 tentin Ver: 2:1	6.16e-48 509.00 52.6% 35.0% 25.0%
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pplication 62147 62147 107ANNONI, 17ANKSLEY, VREBALO, NOENSIE, ENTION: NO CE: TAMK, 2 CE: TAMK, 3 CE:	ty:
ULT I  00-614-408-6 equence 6, Application US/096 atent No. 6762347 ENERAL INFORMATION: ENERAL INFORMATION: APPLICANT: GTOVANNONI, JAMES APPLICANT: TANKSLEY, STEVEN APPLICANT: WEBALOV, JULIA APPLICANT: WEBALOV, JULIA APPLICANT: WEBALOV, JULIA ETILE OF INVENTION: NOR GENE FILE REFERENCE: TANK:213 CURRENT APPLICATION NUMBER: U CURRENT FILING DATE: 2000-07 PRIOR PILING DATE: 1999-07-12 NUMBER OF SEQ ID NOS: 7 SOFTWARE: PATENTIN OF SEQ ID NOS: 7 INFORMATE: PATENTIN OF SEQ ID NOS: 7 ILENGTH: 1209 TYPE: DNA ORGANISM: TOMATO ORGANISM: TOMATO	s: ity: lari
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LT 1  quence 6, tent No. tent No. PERAL INF. PPLICANT: PPLICANT: PPLICANT: ILE REFRIGANT: ILE REFRIGANT: URRENT APPLICANT: URRENT APPLICANT: URRENT FI URREN	nt S O.: Sim cal atch
REGULT 1 Sequence 6, Application US/09614408 Patent No. 6762347 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: GIOVANNONI, JAMES APPLICANT: TANKELEY, STEVEN APPLICANT: TANKELEY, JULIA APPLICANT: WEBALOV, JULIA APPLICANT: WEBALOV, JULIA APPLICANT: WEBALOV, JULIA APPLICANT: NURBELOV, JULIA CURRENT: FILLE REFERENCE: TANK:213 CURRENT APPLICATION NUMBER: US/09/CURRENT FILING DATE: 2000-07-12 PRIOR FILING DATE: 1999-07-12 NUMBER OF SEQ ID NOS: 7 SEQ ID NO 6 LENGTH: 1209 TYPE: DATA TYPE: DATA ORGANISM: TOMATO SCO-614-408-6	Alignment Scores: Pred. No.: Score: Percent Similarity: Descret Local Similarity: Duery Match:
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US-10-780-703-2 (1-379) x US-09-614-408-6 (1-1209)

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LysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLysAlaThr 135
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516 AACAAAAAGGATCTTTGAGGCTAGATGATTGGTTTTATGTCGAATTTACAAGAAGAT
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                                 APPLICANT: NOENSIE, FREDERICK
TITLE OF INVENTION: NOR GENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: TAMK.213
CURRENT APPLICATION NUMBER: US/09/614,408
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,357
PRIOR APPLICATION NUMBER: 60/143,357
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTING UP.C: 2.1
SEQ ID NO 1
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ProGlyPheArgPheHisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLys
                CCGGGGTTTCGATTCCACCCGACGGACGGAGGAACTCATCGTCCACTACCTCAAAAAAAGGA
                                                        ValGluGlyIvsArgPheAsnValGluLeuIleThrPheLeuAspLeuTyrArgTyrAsp
                                                                        GlnHisHisSer-----SerSerSerAsnHisSerAsnAsnLeuAsnAsn
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US-09-614-408-1
US-09-614-408-1
; Sequence 1, Application US/09614408
; Patent No. 6762347
; GENERAL INPORMATION:
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516 AACAAAAAAGGATCTTTGAGGCTAGATGATTGGGTTTTÄTGTCGAATTTÄCAAGAAGAAT 575
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864 AATACAAAAGGTTTCCTTGTTGAGAACAACGAGGACGATGGACTTAAC-----ATGAA
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; Sequence 3, Application US/09533029
; Patent No. 6664446
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
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APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
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APPLICANT: TANKSLEY, STEVEN
APPLICANT: TANKSLEY, STEVEN
APPLICANT: PADMANBHAN, VEERARGAVAN
APPLICANT: PADMANBHAN, VEERARGAVAN
APPLICANT: PADMANBHAN, VEERARGAVAN
APPLICANT: WREBLOV, JULIA
APPLICANT: WHITE, RULIA
APPLICANT: WHITE, RULIA
APPLICANT: WHITE, RULIA
APPLICANT: WHITE, RULIA
CURRENT APPLICATION NUMBER: US/09/614,981
CURRENT APPLICATION NUMBER: US/09/614,981
CURRENT FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 1211
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; Patent No. 6787687
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AAAGCTTTGGTGTTTTTACATCGGAAAAGCTCCTAAAGGTACTAAAAACCAATTGGATCATG 409
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APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Ca-Zhong
APPLICANT: Jiang, Ca-Zhong
APPLICANT: Warsha
APPLICANT: Discase-Induced Polynucleotides
TITLE OF INVENTION: DISEase-INDUCED POLYNUCLEOTIDES
TITLE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                 3.17e-46
494.00
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US-09-533-029-3
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Best Local Similarity:
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LENGTH: 1212
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APPLICANT: Stang, Canes
APPLICANT: Tong, Coliver
APPLICANT: Ratcliffe, Coliver
APPLICANT: Pigrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SEQ ID NOS: 121
SEQ ID NO 37
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APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
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Zhang, James
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COTHER INFORMATION: G502
US-09-533-029-37
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Best Local Similarity:
Query Match:
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130 GlyTyrTrpLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProlle 149
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                                                                                                                                             90 ArgTyrAspProTrpGluLeuProAlaMetAlaAlaIleGlyGluLysGluTrpTyrPhe 109
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17 AACGAAGAAGAGATTTTCCAAGAGCAACAGACAAGAAGAAGAGAAGAGAGTCGGAGCTA 76
                                                                                                                                                                                                                   70 ArgArgLysValGluGlyLysArgPheAsnValGluLeulleThrPheLeuAspLeuTyr
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                                                                                                                       51 ---ValMetProGlyPheArgPheHisProThrGluGluGluLeuIleGluPheTyrLeu
                                                    --АТААБРАБРНІ ВАВРНІ ВАБРМЕТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
                  US-10-780-703-2 (1-379) x US-09-533-029-121 (1-1216)
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APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
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APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Ratcliffe, Oliver
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APPLICANT: Broun, Pierre
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                                 CTGGATGATTGGGTTCTCTGCCGGATTTACAACAAAAAGGAGCTACCGAGAGGCGGGGA 721
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APPLICANT: Aceber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REPERENCE: MB1-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
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-----GluileSerLeuCysArgValTyrLysArgProGl
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddis, James
APPLICANT: Pineda, Omaira
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ORGANISM: Arabidopsis thaliana
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Yu, Guo-Liang
Ratcliffe, Oliver
Pilgrim, Marsha
Jiang, Cai-Zhong
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Samaha, Raymond
Zhang, James
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Sequence 1, Application US/09889926

Sequence 1, Application US/09889926

Sequence 1, Application US/09889926

Patent No. 684486

GRERAL INFORMATION:

APPLICANT: Chua, Nam-Hai

APPLICANT: Chua, Nam-Hai

APPLICANT: Institute of Molecular Agrobiology, The National U

TITLE OF INVENTION: INVOLVED IN COTYLEDON AND LATERAL ROOT DEVELOPMENT;

TILE REFERENCE: 2248-115

CURRENT APPLICATION NUMBER: US/09/889,926

CURRENT FILING DATE: 2001-08-18

NUMBER OF ESQ ID NOS: 2

SOFTWARE: Patent In Ver: 2.0

SEQ ID NO: 2.0
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           BLeuSerThrGluTyrSerGlyAspGly
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US-09-889-926-1
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EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 23
LENGTH: 914
                                                                                             ORGANISM: Arabidopsis thaliana
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US-09-533-029-23
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Alignment Scores:
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LENGIH:
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                                                                                                                                                                                                                                                                                                                                   227 AlaLeuArgGlnGlnGlnHisHisSerSerSerAsnHisSerAsp-----AsnAsn 244
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                                                                                          551 TCTCTGAGCTCT---CCAAAGGAAGACTGGGTCTTGTGTAGGGTATTCCATAAGAATACG
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                                          181 GluThrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLysArg--
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APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Reuber, Lynne
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT APPLICATION NUMBER: 60/125,814
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.1
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Keddie, James
Pineda, Omaira
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APPLICANT: Ratcliffe, Oliver
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APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
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APPLICANT: R
APPLICANT: K
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TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indele:
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Patent No. 6664446
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
TYPE: DNA
ORGANISM: Arabidopsis thallana
                                                                                                                               3.45e-31
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Ratcliffe, Oliver
Pilgrim, Marsha
Jiang, Cai-Zhong
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Zhang, James
                                                           OTHER INFORMATION: G511
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                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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124 AsnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAlaAspArg----MetlleArg 142
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Matches:
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Best Local Similarity:
Query Match:
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                                 ; TYPE: DNA
; ORGANISM: Tomato
US-09-614-408-7
                                                                                                    Alignment Scores:
Pred. No.:
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APPLICANT: TANKSLEY, STEVEN
APPLICANT: TANKSLEY, JULIA
APPLICANT: TANKSLEY, JULIA
APPLICANT: WEBALOV, JULIA
APPLICANT: NOENSIE, FREDERICK
TITLE OF INVENTION: NOR GENE COMPOSITIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: TAMK:213
CURRENT FILING DATE: 1900-07-12
PRIOR APPLICATION NUMBER: 60/143,357
PRIOR APPLICATION NUMBER: 60/143,357
NUMBER OF SEO ID NOS: 7
SOFTWARE: PATENTIN US: 7
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     US/09/533,029
CURRENT APPLICATION NUMBER: US/09/533,025
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SEQ ID NO 115
LENGTH: 1332
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Patent No. 6762347
GENERAL INFORMATION:
                                                                                                                                    TYPE: DNA ORGANISM: Arabidopsis thallana
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330.00
55.7%
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US-09-533-029-115
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Best Local Similarity:
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Pred. No.:
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Sequence 336, Application US/09248796A

Sequence 336, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NOS: 28208
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                                                                                                          159 rGlyLygAlaProLygGlyThrArgThrSerTrplleMetAsnGluTyrArgLeuProHi 179
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                                                             sHisGluThrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLysArgPr 199
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     378 AGGTGATCAGCAGATGAGAAAAACGAAATCTGGGTTTTTGGAAGAGTACTGGCAGACCAAA 437
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Patent No. 6664446
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APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
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ORGANISM: Arabidopsis thaliana
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Mismatches:
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FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 1192
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Sequence 1192, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
ATTLEAMT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AGCAGCAGCAGC 40
                                                                                                                                           Sequence 12547, Application US/09270767

Requence 12547

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFUTARE: Patentin Ver. 2.0
SEQ ID NO 12547
LENGTH: 934
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Matches:
Conservative:
Mismatches:
Indels:
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; ORGANISM: Drosophila melanogaster
US-09-270-767-12547
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US-09-270-767-12547
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Search completed: April 6, 2006, 10:02:43 Job time : 249 Becs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

April 6, 2006, 09:54:37; Search time 4958 Seconds (without alignments) 3576.503 Million cell updates/sec

Run on:

US-10-780-703-2 2034 score: Title: Perfect sc Sequence:

1 MAIVSSTISIIPMSNQVNNN..........MWNPIVPDGNRDHYTNIPFK 379

**BLOSUM62** Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

41078325 segs, 23393541228 residues Searched:

82156650 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=x1h
-Q=/abss/ABSSWEB spool/US10780703/runat\_06042006\_101339\_6361/app\_query.fasta\_1
-Q=/abss/ABSSWEB spool/US10780703/runat\_06042006\_101339\_6361/app\_query.fasta\_1
-DB=EST\_OFWT=fastap -SUFPIX=p2n.rst\_-MTWATCH=0.1.-LOOFCL=0\_LLODFEXT=0
-UNITS=bits -START=1 -END=1. MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFPYT=pto -NORM=est\_ +BEAPSIZE=500 -MINLRN=0 -MAXLENS=2000000000 -HOST=abss03h
-USER=US10780703 @CGN 1 1.5315\_@runat\_06042006\_101319\_6361 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBALOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOR=6 -FGAPEXT=7 -DELEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6

gb\_est1:\*
gb\_est2:\*
gb\_est3:\*
gb\_htc:\* EST: \* Database :

gb\_est4: \*
gb\_est6: \*
gb\_est7: \*
gb\_gss1: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		25	25	7	85	7.	19	72
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SUMMARIES	QI	DR749909	DR749910	AV827617	DR938316	AW683672	BE204243	DR935181
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	* Query Match Length DB	947	901	622	880	648	653	906
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## ALIGNMENTS

RESULT 1

	DR749909 947 bp mRNA linear EST 19-JUL-2005	85-L020254-065-002-E11-SeLA MPIZ-ADIS-065d	CDNA clone 002-E11, mRNA sequence.	DR749909	DR749909.1 GI:71035249	BST.	Arabidopsis thaliana (thale cress)	1 Arabidopsis thaliana	<pre>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;</pre>	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	1 (bases 1 to 947)	Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, B.,	<pre>Gilmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R.,</pre>	Coupland, G., Martin, C., Angenent, G.C., Baeumlein, H., Mock, H.P.,	Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P.,	Droege-Laser, W., Gatz, C., Kavanagh, T., Kushnir, S., Zabeau, M.,	Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S.,	Somssich, I., Weisshaar, B. and Traas, J.	REGIA, an EU project on functional genomics of transcription	factors from Arabidopsis thaliana	Comp. Funct. Genomics 3 (2), 102-108 (2002)	Contact:	Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sabl	owski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli,	Engstroem, Droege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth	, Ruberti, Smeekens, Somssich, Weisshaar, Traas	Bielefeld University, Institute for Genome Research	Universitaetsstrasse 25, D-33594 bieleield, Germany
DR749909	rocus	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	•			REFERENCE	AUTHORS		•					TITLE		JOURNAL	COMMENT						

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Meanli, Mernalweislenbaareuni-bielefeld.de
Meanli, Mernalweislenbaareuni-bielefeld.de
Meanli, Gad detected devinitylas undecemnined frame; Translution: no
Data analysis performed in the frame of RRGULANDRE (Exploiting
regalacors of reproductive development and physiological
performance), a Triateral Corperation in Plant General
Spain (WAT): France (GRODLANDRE) and General (Mail Coordinate by
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Spain (WAT): France (GRODLANDRE) and General (Mail Coordinate by
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All All Coopling of the terms used to describe the quality of the clone:
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The house and clustered and ancient of the sequences
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percent of the sequence, no similarity; not the sequence partial and than 54
percent of the sequence, no similarity; not the sequence were colle
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DR749910
85-L020255-065-002-E11-SeLB MPIZ-ADIS-065d Arabidopsis thaliana
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                            US-10-780-703-2 (1-379) x DR749909 (1-947)
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98.6%
73.6%
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/clone_lib="MPIZ-ADIS-065d"
/note="Weetor: pDONR201; In the context of the EU-funded project REGIA (QLG-CT11999-00876, coordinator Javier Paz-Ares), a set of transcription factor ORFs was generated. The ORFs were produced in a decentralized way in the labs of the participants Most-of the ORPs were generated by RT-PCR using CDNA from various A. thaliana tissues as a template. Initially, it was planned to use yeast recombination to move the ORFs from the cloning vectors into target constructs. For this reason, a number of the clones contain 'REGIA tags' (RG_tag1: 5pr-AATTCCAGCTCACAC-3pr; RG_tag2: 5pr-AATTCCAGCTCACC-3pr; RG_tag2: 5pr-AATTCCAGCTCACC-3pr; RG_tag2: 5pr-AATTCCAGCTCACC-3pr; RG_tag2: 6pr-AATTCCAGCTCACC-3pr; RG_tag2: 6pr-AATTCCAGCTCACTC-3pr; RG_tag2: 6pr-AATTCCAGCTCACTC-3pr; RG_tag2: 6pr-AATTCCAGCTCACTC-3pr; RG_tag2: 6pr-AATTCCAGCTCACTC-3pr; RG_tag2: 6pr-AATTCCGGGAATCCCGGGAATC-3pr; RG_tag2: 6pr-AATTCCGGGAATCCCGGGAATC-3pr; RG_tag2: 6pr-AATTCCGGGAATCCG-3pr; RG_tag2: 6pr-AATTCCGGGAATCG-3pr; RG_tag2: 6pr-AATTCGGGAATCG-3pr; RG_tag2: 6pr-AATTCGGGAATCGGGAATCGGGAATCGGGAATCGGGAATCGGGAATCGGGAATCGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGGGAATCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 LysThrLeuValPheTyrSerGlyLysAlaProLysGlyThrArgThrSerTrpIleMet
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Intl. case detected

Data analysis performed in the frame of REGULATORS (Exploiting)

Inter-species conservation in promoter sequences to identify

regulators of reproductive development and physiological

performance), a Trilateral Co-Operation in Plant Genomics between

Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by

G. Coupland (Coopland-ad-mpiz-koeln.mpg.de). Authors: Vincent

Thareau (IBP-Orsay UMR&618 CNRS-UBS, thareau-ad-ibp.u-psud.fr) and

Alain Lecharny (URCV-Evry UMR INRA-CNRS-UBVE).

Definition of the terms used to describe the quality of the clone:

The about 2250 sequences from the clone collection were sorted

according to clones and clustered. If more than one contig was

formed, the clone was designated 'Contamination'. The contigs and

singletons were blasted against CDS plus pseudogenes from the

TIGRV5 annotation, and the resulting AGI code is presented if more

than 90 percent identity was found. The sequences were also blasted

against all TIGRV5 introns, and matches longer than 50 pp with 95

percent identity are reported as 'intron found'. The remaining

terms (for SeqAnalysis describe the outcome of the evaluation of the

CDS detected after pairwise alignment with CDS plus pseudogenes

from the TIGRV5 annotation file. The sequences or contigs for which

a full CDS with or without STOP codon was detected, a BLASTP

against all TIGRV5 protein sequence; partial good: better

than 95 percent identity; full good: better than 95 percent identity

over more than 95 percent of the sequence; partial good: better

than 95 percent identity over less than 95

percent of the sequence; no similarity; no hit from BLASTP, note

that the collection contains a few clones for which sequencing was not an encent of the sequences of a partial substitution of a partial substitution of a partial substitution of a partial substitution of a parti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski, Coupland, Martin, Angenent, Baeumlein, Carbonero, Colombo, Tonelli, Engstroem, Proege-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Holdsworth, Sheekens, Somesich, Meisshaar, Traas Bielefeld University, Institute for Genome Research University, Institute for Genome Research Whiversitasse 25, D-33594 Bielefeld, Germany Email: bernad, weisshaar@uni-bielefeld.de frame; Translation: no full cds detected
                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                Davies, B.,
                                                                                                                                                                                                                                                                                                                                                      Totale 1 (Dases 1 to 901)

Paz-Ares, J., Valencia, A., Costantino, P., Vittorioso, P., Davies, E. (Malartin, P., Valencia, A., Costantino, P., Vittorioso, P., Davies, E. (Gulmartin, P., Giraudat, J., Parcy, F., Reindl, A., Sablowski, R., Coupland, G., Martin, C., Angenent, G.C., Bacumlein, H., Mock, H. P., Carbonero, P., Colombo, L., Tonelli, C., Engstroem, P., Laux, T., Hordsworth, M., Ruberti, I., Ratcliff, F., Smeekens, S., Somssich, I., Weisshaar, B. and Traas, J. Ratcliff, F., Smeekens, S., FEGIAF, an EU project on functional genomics of transcription factors from Arabidopsis thaliana

Comp. Funct. Genomics 3 (2), 102-108 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 901 Std Error: 0.00
Seg primer: SelB GTAACATCAGAGATTTTGAGACAC.
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/lab_host="E. coli DH5alpha"
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                                                                                   DR749910.1 GI:71035250
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                                         ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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602

232 542 272

Query Match:         54.74         Indels:         0           DB:         1         Gaps:         0           US-10-780-703-2 (1-379)         x AV827617 (1-622)         1           QY	Qy         168 ThrSerTrpIleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGlnLys 187           Db         243 ACTAGTTGGATCATGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAG 302           Qy         188 AlaGluIleSerLeuCysArgValTyrLysArgProGlyValGluAspHisProSerVal 207           Db         303 GCTGAAATACATTGTGCCGAGTGTACAAAAGGCCAGGAGTATCATCCTCTGGTA 362           Qy         208 ProArgSerLeuSerThrArgHisHisHisAshSerThrSerSerThrSerSerThrGGTA 362           Db         363 CCACGTTCTCTCTCTCCACAGACATCATAACCATCATCACCATCATCCCTTTAGCC 422           Qy         228 LeuAstGlinGlinGlinGlinHisHisSerSerSerAshBahashBahashBahash 247           Qy         228 LeuAstGlinGlinGlinHisHisSerSerSerSerAshHisSerAspAshBahashBahash 247	Db 423 TTAAGACAACAACACTTCTCTCTCTATTCTCTCTCTTTAACAAC 482  Oy 248 AsnasnAsnledanAsnasnLeddluysLeuSerThrGlutysEarGlyAspGlySerThr 267  Db 483 AACAACAACAACTCGAGAAGCTCTCCACCGAATATTCCGGCGACGCACA 542  Oy 268 ThrThrThrThrThrAsnSerAsnSerAsnSerAsnSerAsnSerAsnGlnAsnIle 287  Oy 268 ThrThrThrThrThrAsnSerAsnSerAsnSerAsnSerAsnGlnAsnIle 287  Oy 268 ThrThrThrThrThrAsnSerAsnSerAsnSerAsnCartaCattCCATTGCCAATCAAAACATA 602  Oy 288 TyrArgBrowetProTyr 293  Oy 288 TyrArgBrowetProTyr 293  Db 603 TATCGTCCAATGCCTTAC 620  RESULT 4  DRS38316  RESULT 4  DRS38316  RESULT 4  DEFINITION EST1129855 Aquilegia cDNA library Aquilegia formosa x Aquilegia	pubescens cDNA clone DR938316.1 GI-717076 EST. Aquilegia formosa x Aquilegia formosa x Bukaryota; viridiplar Spermatophyta; Magnol Ranunculacea; Aquile I (bases 1 to 880) Hodges, S.A., Rensink, Nordborg, M. and Tomk Generation of ESTS in Unpublished (2005) Other ESTS: EST11298 COntact: Scott Hodges Department of Ecology University of Califor Santa Barbara (2013)
	AV827617 AV8	Onno, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.  and Shinozaki, K.  Large scale analysis of Arabidopsis full-length cDNA (2002b)  JOURNAL Unpublished (2002)  CONTACT: Morcaki Seki  Plant Functional Genomics Research Group  RIKEN Genomic Sciences Center  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  Tel: 81-298-36-4359  Fax: 81-298-36-4359  Fax: 81-298-36-4359  Fax: 81-298-36-4369  Email: msekidortc.riken.go.jp  An Arabidopsis full-length CDNA library was constructed essentially as reported previously (Seki et al., 1998) cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This  cloné is in a modified pBluescript vector. Please visit our web  site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further	FEATURES  Location/Qualifiers  1623  /organism="Arabidopsis thaliana" /mol_type="mRNA" /dol_type="mRNA" /dol_xref="raxon:3702" /clone="RAFL09-17-121" /dow stagge="plants at various developmental stages from germination to mature seeds" /lab_host="Blants at various developmental stages from germination to mature seeds" /lab_host="Blants" /clone lib="RAFL0" /clone lib="R

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648 bp mRNA linear EST 15-JUN-2000
NF017D07LF1F1061 Developing leaf Medicago truncatula cDNA clone
NF017D07LF 5', mRNA sequence.
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
Contact: May GD
                                                                                                                                                                                                                                                                                                                                                                   616 GCATACGATAGCAACAACTCACCGCAACTACTACTACTACTACTACTACTGAGATG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 GATAGCCAATGTTTCTCCAATGATCAGTTCCGCAGTATTGTCACAGCTTCAACCATTGAG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AspThr-----SerAsnAsnThrLeu-----IleValSerThrArgAsnHisGln 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 AspGlyAlaThrTeuMetProGlnThrGlnAlaAlaLeuAlaMetAsnMetIlePro 348
     127 CCTCAGCAAGACACTGATAGATACCAAAAGGCAGAAATTTCGCTTTGTCGAGTCTACAAG 486
                                                  198 ArgProGlyValGluAspHisProSerValProArgSerLeuSerThrArgHisHisAsn 217
                                                                                                                                             218 HisAsnSerSerThrSerSerArgLeuAlaLeuArgGlnGlnGlnHisHisSerSer 237
                                                                                                                                                                                            ------rcarcaaga 555
                                                                                                                                                                                                                                                                                                                                         256 LysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThrThrAsnSerAsn 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 AspAspAspGluThrAlaIleValAspAspLeuGlnArgLeuValAsnTyrGlnIleSer 328
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                            556 GGAACTCAGCCGGATAAAAGACAGCAGAACCTGATCACTTATGGAATTTCAAGCTTTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                         276 SerAspValThrIleAlaLeuAlaAsn-----GlnAsnIleTyrArgProMetProTyr
                                                                                                                                                                                                                                            238 SerAsnHisSerAspAsnAsnLeuAsnAsn-----АвпАвпПеАвпЛенGlu
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 224 6692
Fax: 580 224 6692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 AGACCTGGAGTAGAAGACCACGCCAGAGTTCCCGGCTCC
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Insert Length: 648 Std Error: 0.00
Plate: 017 row: D column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.
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AW683672
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//done lib="Aquilegia cDNA library"
//note="Vector: pCNV SPORT6.1; Site 1: ECORI; Site 2: NotI;
// F2, F3, and F4 lines of Aquilegia Formeax A. Pubescens
were grown from seed in greenhouses at UC Santa Barbara.
From these plants three sets of tissue were collected: 1)
Small flower buds (*10 mm) and very young inflorescences
(71 & 29% by weight respectively), 2) Medium (7-20 mm) and
large (at or near anthesis) flower buds (65 & 35% by
weight respectively) and 3) Shoot apical meristenms. A
fourth set of tissue was collected from plants of A.
formosa. These plants were grown from seed in sand and at
approximately I month root tissue and leaf tissue of
various developmental stages were collected (84 & 16% by
weight respectively). Total RNA was extracted from each
set of tissue and pooled in the following proportions:
1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
total RNA, mRNA was extracted and enriched for full-length
messages and then normalized with proprietary methods by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCCAACCAAGAAGAAACTCATTGAATTCTATCTCCGCCGTAAGGTTGAGGGCAAGCGC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 CGCAACGGAGATCGCCCTAACCGGGTGACATCTGGCTACTGGAAGGCTACTGGTGCA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProHisHisGluThrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLys 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 AlaMetalaalaileGlyGluLysGluTrpTyrPheTyrValProArgAspArgLysTyr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAla 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 AspArgMetIleArgSerGluThrSerArgProIleGlyLeuLysLysThrLeuValPhe 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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                                                                                                                                                                                                              /tissue type="mixed shoot and floral apical meristems, flower buds, leaves and roots" 
lab_host="DH10B T1 (T1 and T5 phage resistance)"
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(db_xref="taxon:338618"
/clone="COIPM65"
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186
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Matches:
Conservative:
Mismatches:
Indels:
Pax: 805 893 472,
Email: hodges@lifesci.ucsb.edu
Seq primer: M13 Reverse.
Location/Qualifiers
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56.5%
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Best Local Similarity:
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/note=_Wector: pBluescript SK -; Site 1: BcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                           1 (bages 1 to 653)
vandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: VandenBoach K
Contact: VandenBoach K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
Texas AkW University. name:T264015e
TiGR sequence name:MTGAP77TK
More information is available at.
http://chrysis.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                            ESTs from uninoculated seedling roots of Medicago truncatula
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Medicago truncatula
Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerAsnHisSerAspAsnAsnLeuAsnAsnAsnAsnAsnIleAsnAsnLeuGluLysLeu 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAACTGAAGAAGAACTTGTAGAGTTCTACCTTCGCCGTAAGGTCGAGGGAAAACGTTTC 123
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                                  /tissue_type="leaf"
/dev_stage="Pooled developmental"
/clone_lib="Developing leaf"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
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[lower buds]

[lower buds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR935181

EST1126720 Aquilegia CDNA library Aquilegia formosa x Aquilegia pubescens cDNA clone CO1P234, mRNA sequence.

DR935181. GI:71704544
                                                                                                                  128
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                                                                                                                                                                                                                                                            SerGlyTyrTrpLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgPro 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlulleSerLeuCysArgValTyrLysArgProGlyValGluAspHisProSerValPro 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquilegia formosa x Aquilegia pubescens
Aquilegia formosa x Aquilegia pubescens
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, Ranunculales;
Ranunculaceae, Aquilegia.
                                                                                                                                                                                         374
                                                                                                                                                                                                                                                                                                               494
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435 ATTGGACTCAAGAAACCCTAGTTTTCTATTCTGGAAAAGCTCCTAAAGGGCATCCGAACC
                                                                                                                                                                                         315 TTTTATGTGCCTCGAGATAGGAAGTATCGAAACGGTGATCGTCCAAATCGTGTAACAACT
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Cother_ESTs: EST126719
Contact: Scott Hodges
Department of Ecology, Evolution and Marine Biology
University of California, Santa Barbara
Tel: 805 893 7813
Fax: 805 893 4724
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/mol_type="mRNA"
/db_xref="taxon:338618"
/clone="CO1P234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 ArgSerLeuSer -- ThrArg-HigHigAsnHigAsn 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hodges@lifesci.ucsb.edu
Seg primer: M13 Reverse.
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formosa. These plants were grown from seed in sand and at approximately 1 month root tissue and leaf tissue of various developmental stages were collected (84 & 16% by weight respectively). Total RNA was extracted from each set of tissue and pooled in the following proportions: 1.5% from sets 1 & 2, 1% from sets 3 & 4. From the pooled total RNA, mRNA was extracted and enriched for full-length messages and then normalized with proprietary methods by

ORIGIN	IGIN	methods by
Alignmen Pred. No Score: Percent Best Loc Query Ma DB:	Alignment Scores: 3.91e-81 Length: 906 Pred. No.: 877.00 Matches: 174 Score: 977.00 Conservative: 25 Best Local Similarity: 64.9* Mismatches: 35 Query Match: 8 Gaps: 5	
US-10-78	6	
δλ Dp	38 GInAenGluaspGlualaAspAspHisAspHisAspMetValMetProGlyPheArgPhe	heArgPhe 57            CCGTTTT 202
ò	58 HisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLysValGluGlyLysArg	77
qq	m	0
රු සි	78 PheAsnValGluLeulleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuPro 	luLeuPro 97              GCTTCCA 322
, o	σ.	Tyr 11
a a	323 GCATTAGCTGCCATTGGAGAGAAAAAATGGTTCTTCTATGTGCCACGAGACC	GAAATAT 382
o o	118 ArgasnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLy8AlaThrGl 	aThrGlyAla 137              CTACTGGTGCA 442
ογ	138 AspArgMet1leArgSerGluThrSerArgProIleGlyLeuLysLysThrLeuValPhe	euValPhe 157
qq	443 GACAGAATGATCCGAAATGATAACTTGAGATCCATTGGGCTTAAGAAGACACTAGTCTT	TAGICTIC 502
6 6	158 TyrSerGlyLysalaProLysGlyThrArgThrSerTrpIleMetAsnGluTyrArgLeu	
α Ω	503 TATTCCGGGAAAGCACCTAAAGCATCAGAACCAGTTGGATCATGAGT	ų
& &	178 ProhishisGluThrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTy	allyrLys 197            ctacaag 622
δ	198 ArgProGlyValGluAspHisProSerValProArgSerLeuSerThrArgHi	sHisAsn 2
g	623 AGACCTGGAGTAGAAGACCACGCCAGAGTTCCCGGCTCC	TCT 664
ò	218 HisasnSerThrSerSerArgLeuAlaLeuArgGlnGlnGlnHi:	1nHisHis 234
ορ	665 CATICITCIGCACCATCITCATCAGGGAACTCAGCCGGATAAAGACAGAAACCTG	AGAACCTG 724
δ	235 SerSerSerAsnHisSerAspAsnAsnLeuAsnAsnAsnAsnAsnIleA	eAsnAsnLeu 254
ф	725 ATCACTTATGGAATTTCAAGCTTTCAAGCATACGATAGCAACAACTCA	772
δ	255 GluLysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThTT	hr 272
qq	773	CTGAGATG 805
ολ	273	laLeuAla 283
д	806 GABABGCTGABTGABGCBGABGCBGTBCTBGCBATGBTBCCGGBACTGCTTGGG	crcrraga 865

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

DEFINITION

RESULT 8 DR928151

ACCESSION

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155 CAAAACAACGACGACAAGGATAACCACGACCACGATATGGTCATGCCTGGCTTCCGTTTT
                                                  HisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLysValGluGlyLysArg
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/lab host="mixed shoot and roots" phage resistance)"
/lab host="mixed shoot library"
/clone lib-"Aquilegia cDNA library"
/clone lib-"Aquilegia cDNA library"
/note="Vector: pCNV SPORT6.1; Site 1: ECORI; Site 2: NotI;
P2, P3, and F4 lines of Aquilegia formosa X As pubescens were grown from seed in greenhouses at UC Santa Barbara.
Prom these plants three sets of tissue were collected: 1)
Small flower buds (*10 mm) and very young inflorescences
/la & 29% by weight respectively), 2) Medium (7-20 mm) and large (at or near anthesis) flower buds (65 & 35% by weight respectively) and 3) Shoot apical meristems. A fourth set of tissue was collected from plants of A. formosa. These plants were grown from seed in sand and at approximately 1 month root tissue and leaf tissue of various developmental stages were collected (84 & 16% by weight respectively). Total RNA was extracted from each set of tissue and pooled in the following proportions:
1.5% from sets 1 & 2, 1% from sets 3 & 4. From the pooled total RNA, mRNA was extracted and enriched for full-length messages and then normalized with proprietary methods by traiting the set of the pooled to the proprietary methods by traiting the propriet of the pr
                                                                                                                                                                    EST 02-AUG-2005
                                                                                                                                                                                                                                                                                                                          Aquilegia formosa x Aquilegia pubescens
Aquilegia formosa x Aquilegia pubescens
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; Ranunculales,
Ranunculaceae, Aquilegia.
                                                                                                                                                                 DR928151
EST1119690 Aquilegia cDNA library Aquilegia formosa x Aquilegia
pubescens cDNA clone CO1NO60, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hodges, S. A., Rensink, W., Buell, C.R., Borevitz, J., Kramer, E., Nordborg, M. and Tomkins, J. Generation of ESTs from Aquilegia Generation of ESTs from Aquilegia Unpublished (2005) Other ESTs: EST119689 Contact: Scott Hodges Department of Ecology, Evolution and Marine Biology University of California, Santa Barbara, CA 93106, USA Fal: 805 893 4724 Email: hodges@lifesci.ucsb.edu Email: hodges@lifesci.ucsb.edu Email: hodges@lifesci.ucsb.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Aquilegia formosa x Aquilegia pubescens" (mol Lype="mRNA" (db xref="taxon:338618" (clone="colNo60"
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                                      ATGCCCAATGTT---TCTCCAATG 886.
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           AsnGlnAsnIleTyrArgProMet
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GlnAsnGluAspGluAlaAspAspHisAspHisAspMetValMetProGlyPheArgPhe 57

US-10-780-703-2 (1-379) x DR928151 (1-853)

No.:

DRIGIN

38

1404 bp DNA linear GSS 21-SEP-2004 OSIFCC004254 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL960332. GL960332.1 GI:52375362 GSS. OUTURE STATES STATES STREET ST 198 ArgProGlyValGluAspHisProSerValProArgSerLeuSerThrArgHisHisAsn 217 919 784 TyrserGlyLysAlabroLysGlyThrArgThrSerTrpIleMetAsnGluTyrArgLeu 177 178 ProHisHisGluThrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLys 197 218 HishanSerSerThrSerSerArgLeuAlaLeu-----ArgGlnGlnGlnHisHis 234 274 117 394 137 454 AspargmetileargSerGluThrSerArgProlleGlyLeuLysLysThrLeuValPhe 157 514 574 97 235 SerSerSerAsnHisSerAspAsnAsnLeuAsnAsnAspagaganIleAsnLeu 98 AlametAlaAlaIleGlyGluLysGluTrpTyrPheTyrValProArgAspArgLysTyr ArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAla 737 ATCACTTATGGAATTTCAAGCTTTCAAGCATACGATAGCAACAACTCA------PheasnvalGluLeuIleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuPro 635 AGACCTGGAGTAGAAGACCACGCCAGAGTTCCCGGCTCC-----TCT 255 GluLysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThr 272 Contact: Chen Chen
Department of Bioinformatic
Bejiing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China chenchen@genomics.org.cn Tel: 86-10-80481559 Fax: 86-10-80488676 Email:

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CDNA, mRNA sequence.
CX527114
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                                     /organism="Oryza sativa (indica cu
/mol type="genomic DNA"
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/bxref="taxon:39946"
/clone lib="Oryza sativa Express
/note="Oryza sativa exon trapped
                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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      Class: exon-trapped.
Location/Qualifiers
Rice genomic sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111 TCCATG-GGCAGCTCCGCCGCTGCTGATGAGCTGAGCTCGCTGGTGGGGCCACGGCAC 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1230 TACGACGCCGTCGCCTCAACCAACGCCGGCGCGCTCGGGACGACGACGACGGCGGCGC 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGATCAGCAGCAGCAATTTCAGCAAGACTTCGCGGCGGCATTGTACCAGCAGTACTCC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 AAGAACACGAGCGGTGCCTTCGCCTCCACGTACTCGCTGCTCAACCTCGTCAACGCGGCA 1110
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 623)
Zhang,Y., Chekhouskiy,K., Scott,A.D., May,G.D. and Mian,M.A.R.
Medicago truncatula Aphid Infected Shoot Expressed Sequence Tags
from the Samuel Roberts Noble Foundation - Center for Medicago
                                                                                                                                                                 1290 AGCGGCGACACTGCCGATGTCGCTCGCCGTTCTCCGACAGGATCTGGGACTGGAATAA
rSerSerAsnHisSerAspAsnAsnLeuAsnAsnAsnAsnAsnIleAsnAsnLeuGl
                                                            817 CTCCACCTCCTCAGCAGCGAGTGCACGTCGCCGCCCGCCATCGTCACGGACCACGCCGCC
                                                                                                                            255 uLysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThrAsnSerAs
                                                                                                                                                                                                                                                         275 nSerAspValThrIleAlaLeuAlaAsnGlnAsnIleTyrArg-----ProMetProTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sGlnAspAspAspGluThrAlaIleValAspAspLeuGlnArgLeuValAsnTyr----
                                                                                                                                                                                                                                                                                                                                                                                        293 rAspThrSerAsnAsnThrLeuIleValSerThrArg----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ThrilePro-----ThrilePro------AsnAsnAlaLeuTrpAspMetTrpAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||||
| 1350 TCCGATCCCCGAGGCCGGAGGTAGGATTACAGCACCAGTACTGGATTCAAG 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 nProlleValProAspGlyAsnArgAspHisTyrThrAsnIleProPheLys 379
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/db_xref="taxon:3880"
/tissue_type="Aphid-infected shoots"
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 224 6550
Email: 580 224 6592
Email: 98may@noble.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GlnIleSerAspGlyAlaThr-----
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Gm-c1068-3822 5' similar to TR:Q9ZVP8 Q9ZVP8 PUTATIVE NAM ;,
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Pred. No.:
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                                                                                          ORGANISM
                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
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                      /clone lib="Aphid-Infected Shoots"
/clone lib="Aphid-Infected Shoots"
/note="Vector: Lambda Zap; Medicago truncatula plants were
infested with 300 spotted-aphids each. Tissue samples were
collected by harvesting the entire shoots from 13 plants
after 12, 24, 48, 72 and 96 hours of infestation. Total
RNA was extracted from each sampling time and equal
amounts of total RNA were pooled together for mRNA
purification for CDNA library construction. The CDNA was
directionally ligated into the Uni-Zap XR vector
(Stratagene) and packaged using the Gigapack III Gold
packaging extracts. Phagemids containing CDNA inserts were
using ExAssist helper phage and the E. coli strain
XLI-Blue MRR' (Stratagene). Excised plasmids were plated
using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI893633 SA-JUL-2004 SI6 bp mRNA linear EST 24-JUL-2004 sai68h03.yl Gm-c1068 Glycine max cDNA clone GENOME SYSTEMS CLONE
   stage="harvested after 12, 24, 48, 72 and 96 hours of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAla 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AspArgMetIleArgSerGluThrSerArgProlleGlyLeuLy8Ly8ThrLeuValPhe 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrSerGlyLysAlaProLysGlyThrArgThrSerTrplleMetAsnGluTyrArgLeu 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 CATCCAACTGAAGAAGAACTTGTAGAGTTCTACCTTCGCCGTAAGGTCGAGGGAAAACGT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 AlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyrValProArgAspArgLysTyr 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 GluLysGlyIleGluAspAsnAspHisArgGlyGlyGlnGlu--
                                                                                                                                                                                                                                                                                                             623
151
19
24
3
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Matches:
Conservative:
Mismatches:
Indels:
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802.50
86.3$
76.6$
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Best Local Similarity:
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BI893633
LOCUS
DEFINITION
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90
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.,
Unpublished (1999)
Other ESTS: BUSSO76 corresponding to Gm-r1088-7999 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anote—"Vector: pilueeript II SK+; Site 1: ECORI; Site 2: XhoI; The CDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. ECORI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECORI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Figure 1. Set Wat son. wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTS on Clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stopp: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. :516

Coganiam="Glycine max"

/mol type="mkNA"

/cultivar="Williams 82"

/dub xxef="texon:8847"

/clone="GRNOWE SYSTEMS CLONE ID: Gm-c1068-3822"

/tissue_type="Leaf, drought stressed, 1 month old plants, greenhouse grown"
                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Conservative:
Mismatches:
Indels:
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/clone_lib="Gm-c1068"
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                                                    BI893633.1 GI:16105902
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799.00
96.2$
92.3$
                                                                                                                Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
sequence.
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Best Local Similari
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Query Match: 39.2% Indels: 95 DB: 10 Gaps: 16 US-10-780-703-2 (1-379) x CL971389 (1-1245)	32 GlyGlnGluSerHisValGlnAsnC     :::    :: 40 GGGAGGAAGCGGCGGCCGATCAGG	Qy 47 AspHisAspMetValMetProGlyPheArgPheHisProThrGluGluLeuIleGlu 66 :::::   :::	Oy 67 PheTyrLeuArgArgLysValGluGlyLysArgPheAsnValGluLeulleThrPheLeu 86	Oy 87 AspLeuTyrArgTyrAspProTrpGluLeuProAlaMetAlaAlaIleGlyGluLysGlu 106	107 TrptyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgVal 12	340		460 CGCAGCACCTGGATCATGAACGACTACCCCCCCGCCGCCGCAGACGCCGATCTC 51 185 TyrGlnLygAlaGluIleSerLeuCygArgValTyrLygArgProGlyValGluAsp 20	DD 520 ITCIACAGICIGAGAICICGCICIGCCGCCICICCGCACICCGCACAICGACGACGC 379  Qy 204HiBPROSErValProArgSerLeuSerThr 213	214 ArgHisHisAsnHisAsnSerSerThrSerSerArgLeuAlaLeuArgGlnGlnGlnHis 	234	Oy 254 LeuGluLysLeuSerThrGluTyrSerGlyAspGlySer	Qy 267ThrThrThrThrThrThrAsnSerAsnSerAspValThrIleAlaLeuAlaAsn 284	285 GlnAsn1leTyrArgProMetPro	293 913	Qy 3093spAspAspOluThralaIleValAspAspLeuGlnArgLeuVal 323 :::    ::     bb 973 GCGGCGGCGGCAGTAGCTCGACACTCGAGGTCAGCAGGTGCTGGCGGGCCAC 1032	
Db         49 GACGATAATGATGATCACGAGCACGACATGGTCATGCCCGGCTTTCGCTTCCACCCAACT 108           Qy         61 GluGluGluLeuIleGluPheTyrLeuArgArgLysValGluGlyLysArgPheAsnVal 80	109 GAAGAAGGCTCGTGGAATTCTACCTTCGCCGTAAGGTGGAGGGAAAGCGTTTCAACGTT  81 GluLeulleThrPheLeuAapLeuTyrArgTyrAspProTrpGluLeuProAlaMetAla	DD 169 GAGCTTATTACTTTCCTCGATCTTTATCGCTATGACCCTTGGGAGCTTCCCGCCTTGGCA 228  Oy 101 AlaileGlyGluLysGluTrpTyrPheTyrValProArgAspArgLysTyrArgAsnGly 120	121 ASPARGPROASHARGVALTHINGSEGLYTYTTFDLYSALATHRGTYALAASPARGMSE 	141 IleArgSerGluThrSerArgProlleGlyLeuLysLysThrLeuValPheTyrSerGly	161 LYBATAPPOLYSG1YThrArgThrSerTrp11eMetAsnG1uTyrArgLeuProHisHis	Qy         181 GluthrGluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyr         196           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 12 CL971389 LOCUS CL971389 1245 bp DNA linear GSS 21-SEP-2004 DEFINITION OSIFCC021242 Oryza sativa Express Library Oryza sativa (indica	cultivar-group) genomic, genomic survey sequence. ACCESSION CL971389.1 GI:52397381 KEYWORDS GSS. SOURCE Oryza sativa (indica cultivar-group)	ORGANISM Oryza sativa (indica cultivar-group)  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	AUTHORS Ma,L., Wange,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. TITLE An analysis of transcriptional regulation of the rice genome and	its comparison to Arabidopsis AL Unpublished (2004) Contact: Chen Chen Department of Bioinformatic	Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559 Fax: 86-10-80488676		Fortions   Fortion Quartities   1		Alignment Scores: Pred. No.: 1.36e-72 Length: 1245 Score: 797.50 Matches: 185 Percent Similarity: 55.8% Conservative: 46 Best Local Similarity: 44.7% Mismatches: 88	

the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Prisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"	dgnment S ed. No.: ore: rcent Sim st Local ery Match :	27 27 10 33	Oy 104 GlulysGluTrpTyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArgPro 123	164 LysGlyThrArgThrSerTrplleMetAsnGluTyrArgLeuProHisHisGluThrGlu 18
324	BF625246 LOCUS BF625246 LOCUS BF625246 ACCESSION BF625246		COMMENT ON DEC 18, 2000 this sequence version replaced gi:13082400.  CONTACT: Wing RA  Clemson University Genomics Institute  Clemson University  100 Jordan Hall, Clemson, SC 29634, USA  Tel: 864 656 4228  Fax: 864 656 4228  Email: rwing@clemson.edu  Total hq bases = 583  Seq primer: AATPAACCCTACTACAAAGGG  High muality sequence stop: 691.	FEATURES  1. 694  Organism="Hordeum vulgare subsp. vulgare"  ("Organism="Hordeum vulgare subsp. vulgare"  ("Organism="Morex"  ("Sub species="vulgare"  ("Ab Lot="Warder" laber "Seedling shoot"  ("Jab host="Tutta]  ("Jab host="Tutta]  ("Jone lib="Hordeum vulgare seedling shoot EST library  HVCDNA001 (Cold stress)"  ("Anote="Vector: lambda2AP; Site 1: ECRI; Site 2: Xhoi;  Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatlization dishes. Five-day old seedlings were incubated at Soc for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) CDNA pagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at

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/dav stage="varies by tissue"
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                                                                                                                                                                                                                                                            EST 28-JUL-2005
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y. Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fax: 520 621 9285
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
                                                                                                                                                                                                                                                            313028
__BFb0041P20.r ZM_BFb Zea mays cDNA 5', mRNA sequence.
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clade; Panicoideae; Andropogoneae; Zea.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
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                                                                                      195 ValTyr 196
                                                                                                                                        GTGTAT 524
                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
Zea mays
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Pred. No.:
                                                                                                                                           519
                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCAAGCGCTTCAACGTTGAACTCATTACCTCTCTAGATCTCTATCGCTATGACCCCTGG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 GAGCTGCCTGCCTGGCTGCAATTGGAGAAGGAATGGTTCTTCTATGTGCCCAGAGAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 ArgLysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLysAla 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCAAGTATCGAAACGGGGATCGCCCCAACCGGGTACTGGAACGCAA338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrGlyAlaAspArgMetIleArgSerGluThrSerArgProIleGlyLeuLysLysThr 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 CTTGTTTTCTACTCTGGGAAGGCTCCTAAAGGCCATCCGAACAAGCTGGATCATGAACGAG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluLeuProAlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyrValProArgAsp 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 Acadeadericaricadarcarcedadecerrecececaarrecerraadaacri 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 TyrArgLeuProHisHisGluThrGluLysTyrGlnLysAlaGluIleSerLeuCysArg 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 GlyLysArgPheAsnValGluLeuIleThrPheLeuAspLeuTyrArgTyrAspProTrp 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 GCCAACATGAGCCAAGAAGACAACAAGGATGAGCATGAACATGACATGGTGATGCCTGGC
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                          rosids; Viraceae, Vitis.
1 (bases I to 525)
10ccC,P., Hua,C., Davies,C. and Thomas,M.R.
Expressed sequence tags from the grapevine cultivar Cabernet
                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: pTriplex2 5' primer BD Biosciences BACKWARD: pTriplex2 3' primer BD Biosciences Plate: 0.39 row: B column: 06 Seq primer: pTriplex2 5' primer BD Biosciences High quality sequence stop: 525.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:29760"
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                                                                                                                                                                                                                                                                                       MS200, Reno, NV 89557-0014,
Tel: 775-784-1918
                                                                                                                                                                                              Contact: Cushman JC
Department of Biochemistry
University of Nevada
                                                                                                                                                                                                                                                                                                                                         Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRimers
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782.00
93.8%
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Unpublished (2003)
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AUTHORS
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Matches: 155 Conservative: 29 Mismatches: 57 Indels: 36 Gaps: 5	2 (1-3/9) x DKB1302B (1-801) GlylleGluAspAsnAspHisArgGlyGlyGlnGluSerHisValGlnAsnGluAspGlu 42 	AlaaspasphisasphisaspmetvalmetProdlyPheargPheHisProThrGluGlu 62 	GlubeuileGluPheTyrLeuArgArgLysValGluGlyLysArgPheAsnValGluLeu 82	IleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuProAlaMetAlaAlaile	GlyGluLysGluTrpTyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArg 12:    :::	ProAsnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAlaAspArgMetIleArg 14; 	SerGluThrSerArgProlleGlyLeuLysLyrThrLeuValPheTyrSerGlyLysAla .16. 	ProLysGlyThrargThrSerTrp11eMetAanGluTyrargLeuProHisHisGluThr 18: 	GluLysTyrGlnLysAlaGluIleSerLeuCysArgValTyrLysArgProGlyValGlu 20 :::::           GACCGCTACCAAAAGGAAATTTCTCTTTGCAAAGTGTACAAACGACGAGGGATTGAA 55	AspHisProSerValProArgSerLeuSerThrArgHisHisAsnHis-AsnSerSerTh 22: 	isHisSerSerSerAsn 2		snLeuGluLysLeuSerThrGluTyrSerGlyAspGlySerThrThrThrThrThrTh 27	rAsnSerAsnSerAspValThrIleAlaLeuAlaAsnGlnAsnIle 287 	
α 	x DK813028 (1-801) .spAsnAspHisArgGlyGl          :CGCAGCACGGCGGCGG	spHisAspMetValMe            GACATGGTGAT	neTyrLeuArgArgLy                 ctAccrcccccra	spleuTyrArgTyrAs                 \ccrcTaccgcTACGA	rpTyrPheTyrValPr 	nrThrSerGlyTyrTr 	rgProlleGlyLeuLy 	rgThrSerTrpIleMe   :::             GAGCAGCTGGATCAT	ysAlaGluileSerLe 	alProArgSerLeuSe       CTTTC	AlaLeuArgGlnGlnGlnH       scaaccarggaaaagaagc	Hisser        sacggregcactcar	LeuSerThrGluTyrs       CCATACA	AspvalThrileAlai     GCTCGAGCAGCTACAC	
arity: milarity: -2 (1-379)	1											0	4 :	ra ::	
	US-10-780-703 Qy 23 Db 32	Qy 43 Db 92	Qy 63 Db 137	Qy 83 Db 197	Oy 103 Db 257	Qy 123 Db 317	Oy 143 Db 377	Oy 163 Db 437	Cy 183 Db 497	Oy 203 Db 554	Oy 222 Db 595	Oy 240 Db 655	Qy 252 Db 701	Oy 272 Db 739	

Search completed: April 6, 2006, 13:03:38 Job time : 4969 secs

Perfect score:

ritle:

Sequence:

OM protein

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Scoring table:

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Adx70597 Rice gene
Adx70517 Rice gene
Adx7011 Rice gene
Adx70311 Rice gene
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Adx75780 Plant ful
Add30255 Plant yie
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Adx3141 Bnvironme
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Add55715 Thalecree
Add31002 Plant yie
Adi61478 CDNA enco
Aac43036 Arabidops
Adi42375 Plant tra
Adx10762 Plant tra
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ADA69342
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ADX17043
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 KR2004075252-A.
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ADW23847
     Command line parameters:

-MODELeframe+_pzn.model -DEV=xlp
-G=/abse/ABSSMESE spool/US10780703/runat_06042006_101335_6310/app_query.fasta_1
-G=/abse/ABSSMESE spool/US10780703/runat_06042006_10135_6310/app_query.fasta_1
-DB=N Geneseq -QFMT=fastap -SUPFIX=pzn.rng -MINMATCH=0.1 -LCOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abse05p
-USRR=U310780703_0CGN 1 1 1096_6 munat_06042006 101335_6310 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=0 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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ArgLeuValAsnTyrGlnIleSerAspGlyAlaThrThrLeuMetProGlnThrGlnAla 340
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                                               SerThrSerSerArgLeuAlaLeuArgGlnGlnGlnHisHisSerSerSerAshis
                                                              SeraspasnasnleudsnasnasnasnasnileasnasnleuglulysleuSerThrGlu
                                                                                                                                                                                                     TATTCCGGCGACGCAGCACAACAACAACACACAAACAGTAACTCTGACGTTACCATT
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                                                                                                                                                                                        The present invention relates to the novel gene LOVI (LOng Vegetative phase 1) from Arabidopsis thaliana and its use in controlling flowering time in plants. LOVI inhibits the flowering stimulating gene AGL20. LOVI can be used for manipulating flowering time by over-expressing LOVI to delay flowering, or inhibiting expression of LOVI to stimulate flowering. LOVI is also useful for identifying homologous genes in other plants. The present sequence is the LOVI coding sequence.
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                                                                           New LOVI polynucleotide encoding a polypeptide controlling the flowering time of plants, i.e., either delaying or inducing early flowering of the plants.
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                   Lee
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ArgLeuValAsnTyrGlnIleSerAspGlyAlaThrThrLeuMetProGlnThrGlnAla 340
                                                                                                                                                                                                                                                                               AlaLeuAlaMetAsnMetIleProAlaGlyThrIleProAsnAsnAlaLeuTrpAspMet 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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                                                                                                         TCCGACAACAACCTTAACAACAACAACAACATCAACAATCTCGAGAAGCTCTCCACCGAA
                             TyrSerGlyAspGlySerThrThrThrThrThrAsnSerAsnSerAspValThrIle
                                                                                           AlaLeuAlaAsnGlnAsnIleTyrArgProMetProTyrAspThrSerAsnAsnThrLeu
                                                                                                                                                        IleValSerThrArgAsnHisGlnAspAspAspGluThrAlaIleValAspAspLeuGln
                                                          781 TATTCCGGCGACGCACCACAACAACGACCACAAACAGTAACTCTGACGTTACCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rate; senescence;
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fiang C, Reuber TL, Creelman RA, Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; transcription factor; transgenic plant; growth seed germination rate; plant vigor; seedling vigor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant yield-related polynucleotide clone G962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 112; 454pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA; 1444
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; 2001US-0336049P.
; 2001US-0338692P.
; 2002US-00171468.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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P-PSDB; ADD30084.
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Pilgrim ML,
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                           The present invention relates to Arabidopsis thaliana Long Vegetative phase 1, LOV1, gene (ADX17041), coding sequence (ADX17041) and protein (ADX17042). LOV1 controls the flowering time of plants by repressing the activity of flowering-promoting gene AGL20, and so is useful for controlling flowering: the flowering time of plants can be delayed by LOV1 gene overexpression, or early flowering can be induced by suppressing the expression of the LOV1 gene. The LOV1 gene was isolated from Arabidopsis thaliana by an activation tagging screen.
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                                            1168 GCTCAACAGTTTCATCATACTCAACAACAAATGCTAACGCAAACGCATTACAATTGGTG 1227
                                                                                                                                                                                                                                                                                                                                                                                                          ds; gene; transcription factor; transgenic plant; salt stress resistance; osmotic stress resistance; freezing tolerance; drought tolerance; low humidity tolerance; radiation resistance.
                                                                     IlevalSerThrArgAsnHisGlnAspAspAspGluThrAlaIlevalAspAspLeuGln 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New plant transcription factor polynuclectides and polypeptides, useful in producing transgenic plants with commercially valuable properties,
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ProAspGlyAsnArgAspHisTyrThrAsnIleProPheLys 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "transcription factor"
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Jiang C, Ratcliffe O, Pineda O,
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11-DEC-2001; 2001US-0338692P.
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   modified or altered desirable traits as compared to a reference plant, euch as an alteration in a plant growth characteristic, e.g. growth rate, germination rate of seeds, vigor of plants and seedlings, or leaf and flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the CDNAs of the invention.
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                                                                               Sequence 1444 BP; 490 A; 350 C; 246 G; 358 T; 0 U; 0 Other;
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Matches:
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                                                               The invention relates to a number of isolated cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant transcription factor polymucleotides and polypeptides are useful in producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, e.g. salt stress resistance, osmotic stress resistance, tolerance to freezing, drought, low humidity tolerance, or radiation resistance. Sequence information related to the polymucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention
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an invention can be used to produced a plant having altered traits such as:

an invention can be used to produced a plant having altered traits such as:

altered flower structure, change in stem bifurcations, altered branching pattern, reduced apical dominance, reduced trichome density; lack of trichomes; reduced ectopic trichome development; altered stem morphology; increased root growth; increased root hairs; altered seed development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation or cell differentiation; rapid development; altered cell proliferation in light response or shade avoidance. The biochemistry; increase in root anthocyanins; increase in plant cransgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant transgenic plant, polynucleotides and polypeptides are useful in bioinformatic search methods. This sequence represents a plant
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                                                                                                                                                                                                                                                              New transgenic plant comprising a recombinant polynucleotide of any one of more than 500 nucleotide sequences, useful in bioinformatic search methods.
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                                                                                                                                                                           Haake V;
Keddie J
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Matches:
Conservative:
Mismatches:
Indels:
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O, Adam LJ, Reuber TL,
Pineda O, Yu G;
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Ratcliffe O,
Dubell AN, Pin
                                                 RATCLIFFE O.
ADAM L J.
REUBER T L.
KEDDIE J.
BROUN P E.
PILGRIM M L.
                                        CREELMAN R A
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PINEDA O.
YU G.
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P-PSDB; ADI44013.
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Query Match:
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HEARD J I
HAAKE V.
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Creelman RA,
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     Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide encoding a polypeptide controlling the flowering plants, i.e., either delaying or inducing early flowering of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP, 896 A, 509 C, 388 G, 813 T, 0 U, 0 Other;
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                                                                                   Arabidopsis thaliana LOV1 genomic sequence, SEQ
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Matches:
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                                                                                                                                                                                                                                       "LOV1 protein"
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Flowering; plant; gene;

10-MAR-2005

ADW23849;

Arabidopsis thaliana

Key

\*tag= a number= .622 .2351

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Claim 5; SEQ ID NO 3; 25pp; Korean

3.28e-155 1735.00

Alignment Scores: Pred. No.: Score:

Sequence 2606

Kim

χD,

Choi

Choi EG,

Ahn JH,

WPI; 2005-054880/06. P-PSDB; ADW23848.

time of plants,

plants

New LOV1

20-FEB-2003; 2003KR-00010772 20-FEB-2003; 2003KR-00010772

KR2004075252-A.

27-AUG-2004

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                                                                                                                                                                                                                                   New LOV1 polynucleotide encoding a polypeptide controlling the flowering time of plants, i.e., either delaying or inducing early flowering of the
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                                                                                                                                              (UYSE-) UNIV SEOUL NAT IND FOUND.
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P-PSDB; ADX17042.
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                                                          AsnGlyAspArgProAsnArgValThrThrSerGlyTyrTrpLysAlaThrGlyAlaAsp
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The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or portholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for altering the
an abiotic stress such as cold
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katagiri
                                                                                                                                                                              abiotic stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                  responsive polynucleotide SEQ ID NO:768.
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J, Zhu T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
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  CDNA; 1212
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24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
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T, Provart
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standard;
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Best Local Similarity:
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Moughamer T,
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ACL26812
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Whitham S, Xie Z,
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                                                                                                                                                                                                                                    ArgProlleGlyLeuLysLysThrLeuValPheTyrSerGlyLysAlaProLysGlyThr 166
                                                                                                                                                                                                                                                              CGCCCCATCGGCCTCAAGAAGACGCTCGTCTTCTACTCCGGCAAGGCCCCAAGGGGCGTC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; ss; plant; transcription; gene regulation; gene expression;
transgenic plant; drought resistance; disease resistance; salt tolerance;
cold tolerance; freezing tolerance; flowering; flavor enhancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to novel isolated plant nucleic acid molecules, or
GAGAACGACCTGGTGATGCCGGGGTTCCGGTTCCACCCGACGGAGGAGGAGCTGATCGAG 168
                       86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides isolated from plants encoding transcription factors, and polypeptides encoded by such polynucleotides, useful for regulating gene transcription and gene expression.
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                                                                                                                             TrpTyrPheTyrValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgVal
                        PheTyrLeuArgArgLysValGluGlyLysArgPheAsnValGluLeuIleThrPheLeu
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Gause K,
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Higgins C, Lasham A, Lund
Veerakone S, Westwood C,
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                                                                                                                                                                                                                                                                                                    469 CGCAGCAGCTGGATCATGAACGAGTACCGCTTCCC 504
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Grigor M, 1
Puthigae S,
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P-PSDB; ADW18488.
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Forster RLS, Gr
Phillips J, Put
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variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The present invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably

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linked to the desired nucleic acid to be expressed. It further provides transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height change, enhanced cold, frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others. Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polynucleotide is a plant transcription factor CDNA sequence of the invention.
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                           TyrArgProMetProTyrAsp 294
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AGTACAGATGAAATTGTTAAGCTCGAGGAAATGCCAACAGATATAAAAGTTATGCCAAAA 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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E Z, Zhu T,
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Whitham S, Xie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; bacterial infection;
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7, Quan S,
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                                                                                                                       MetProGlyPheArgPheHisProThrGluGluLeuIleGluPheTyrLeuArgArg
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                                                                                                                                                                                                                                                           AspProTrpGluLeuProAlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyrVal
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The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme cosmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighnin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake, or by providing improved plant growth and development under at least one streams condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert plants can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for
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growth rate; cell cycle pathway; disease resistance; galactomanna production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; proteit; gene; ss.
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oGlyPheArgPheHisProThrGluGluGluLeuIleGluPheTyrLeuArgArgLysVa
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